

459/498

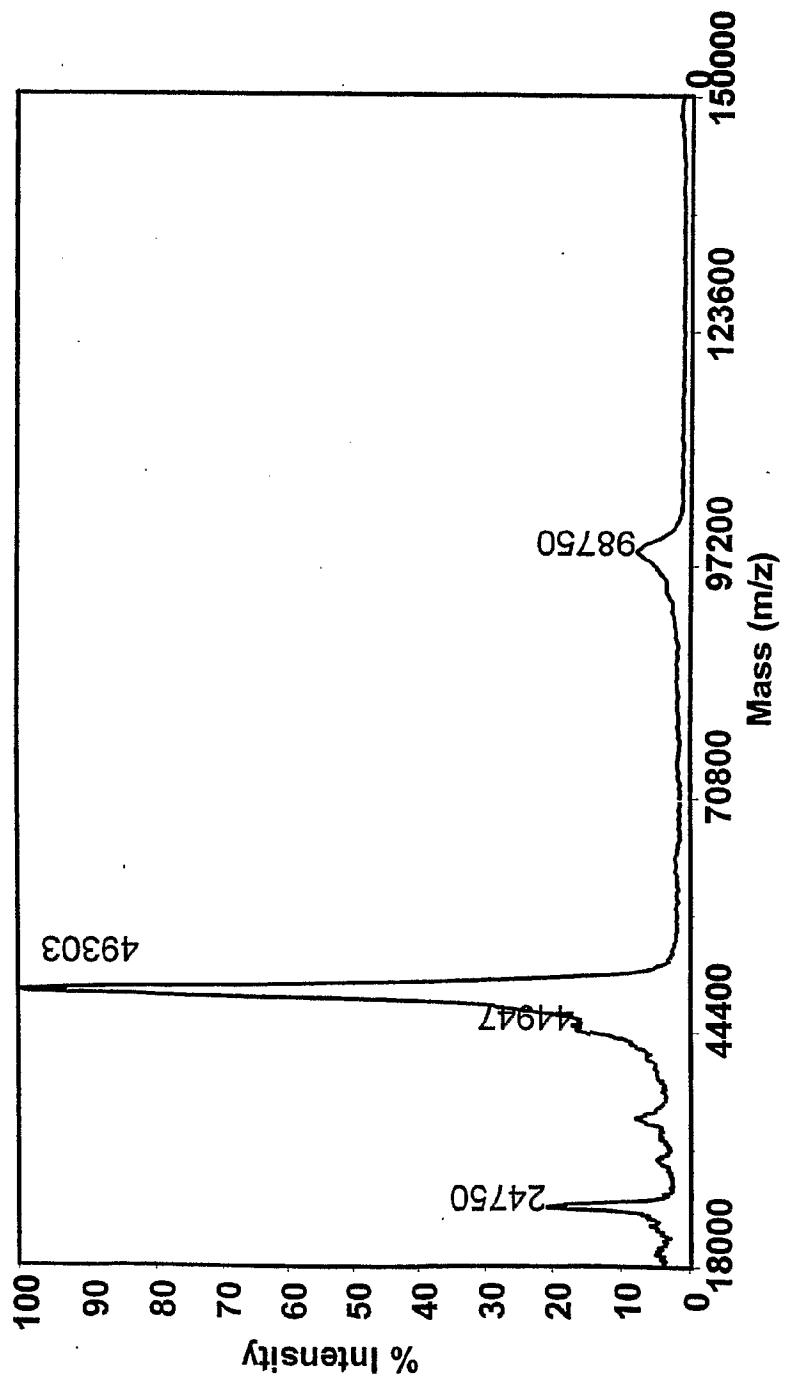


FIG. 158

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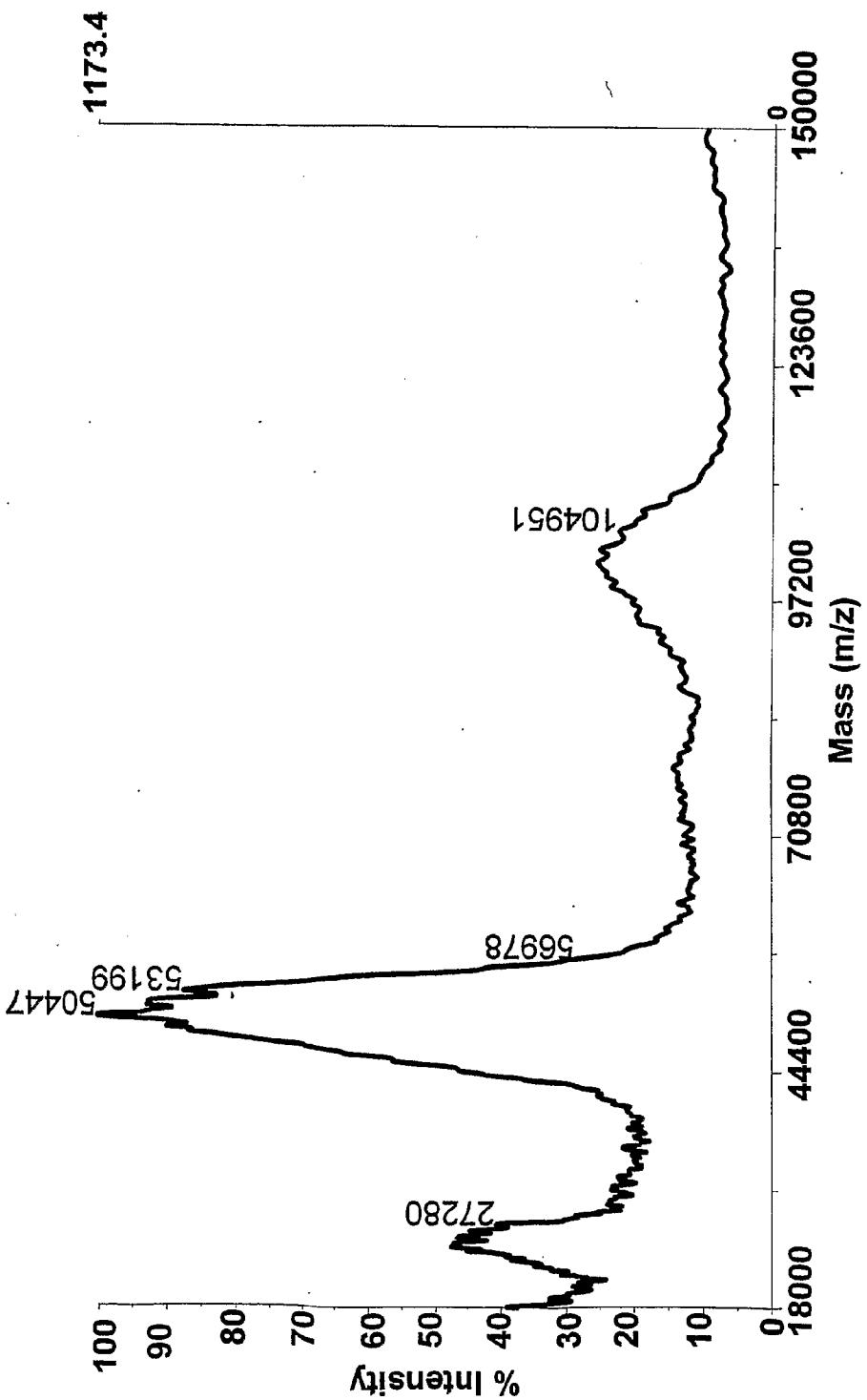


FIG. 159

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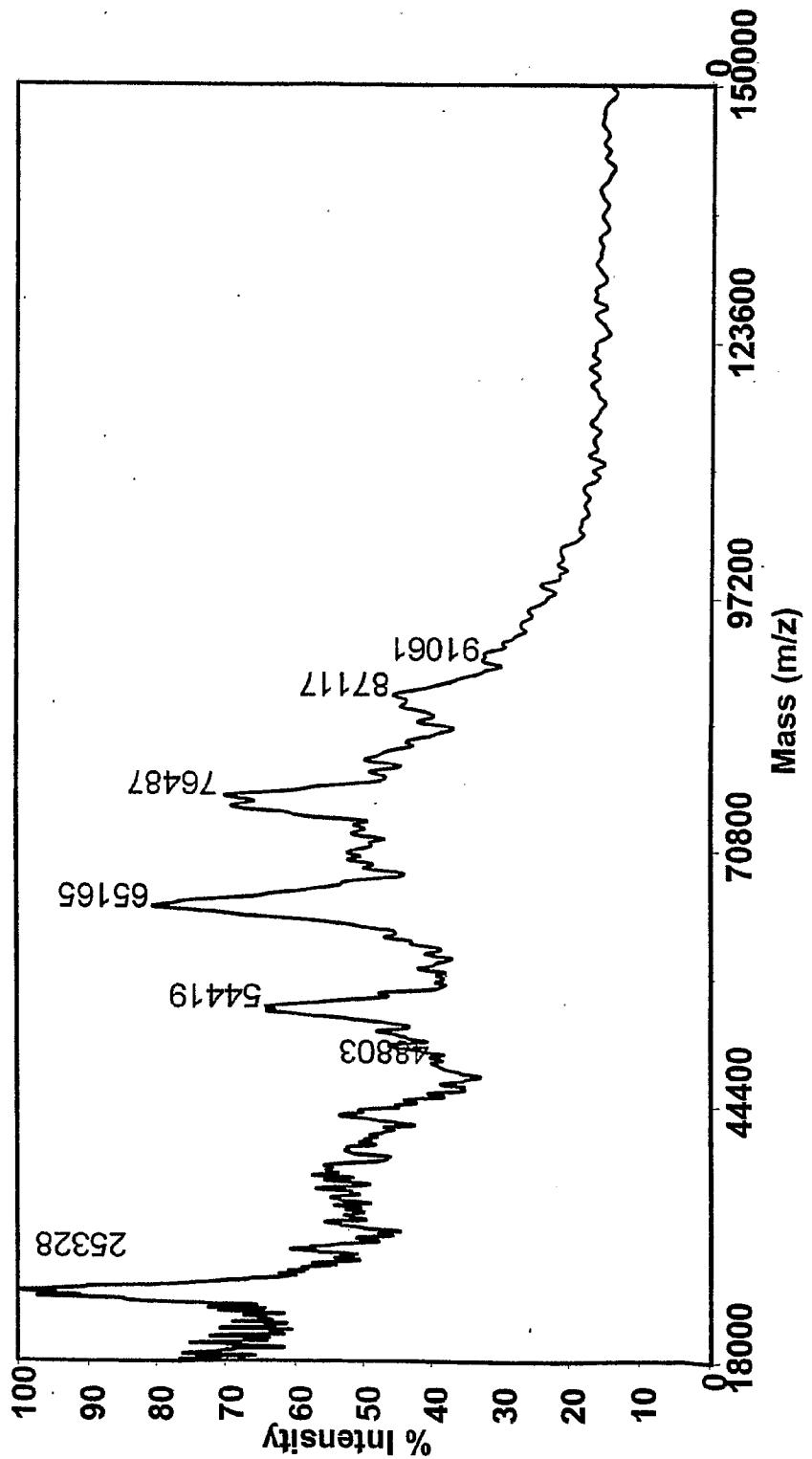


FIG. 160

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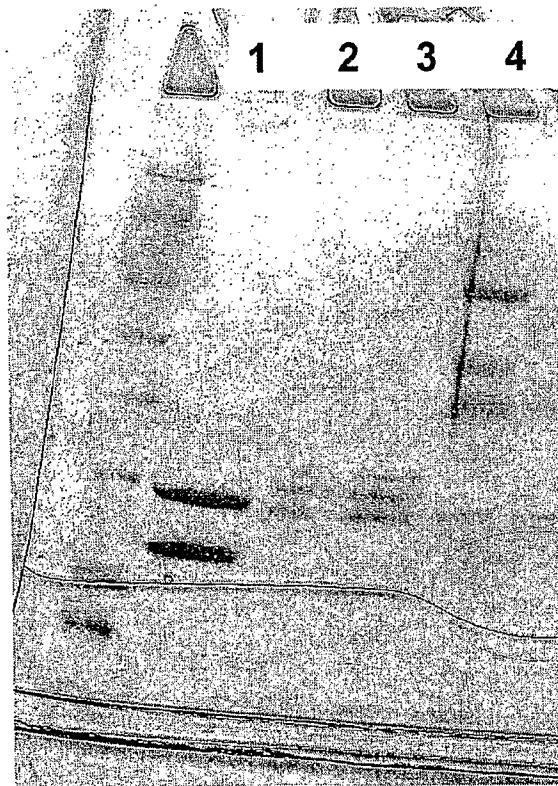


FIG. 161

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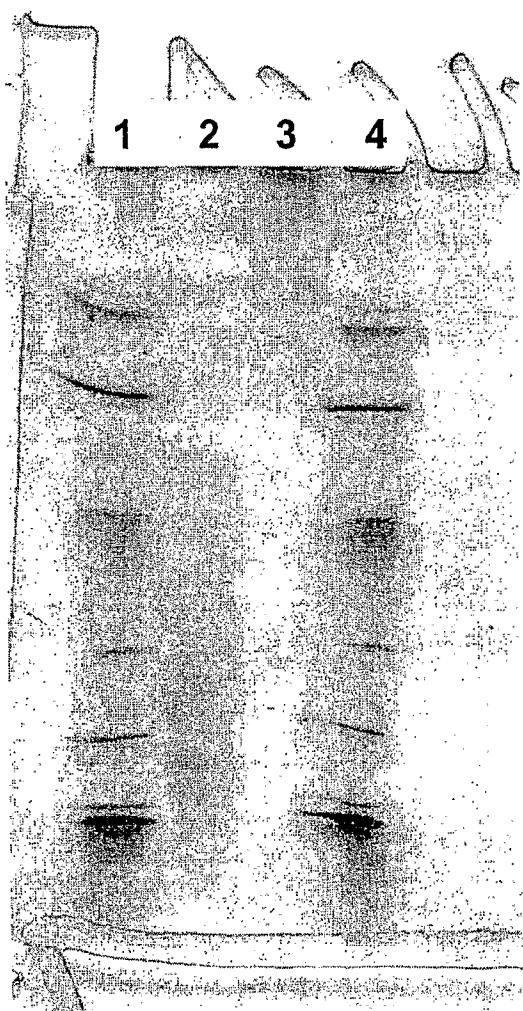


FIG. 162

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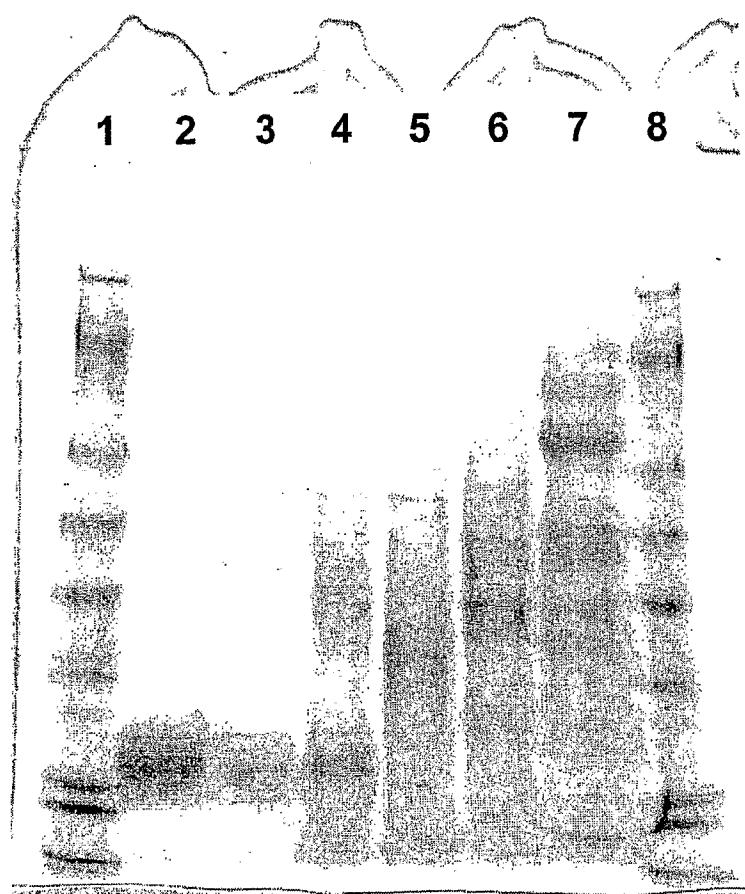


FIG. 163

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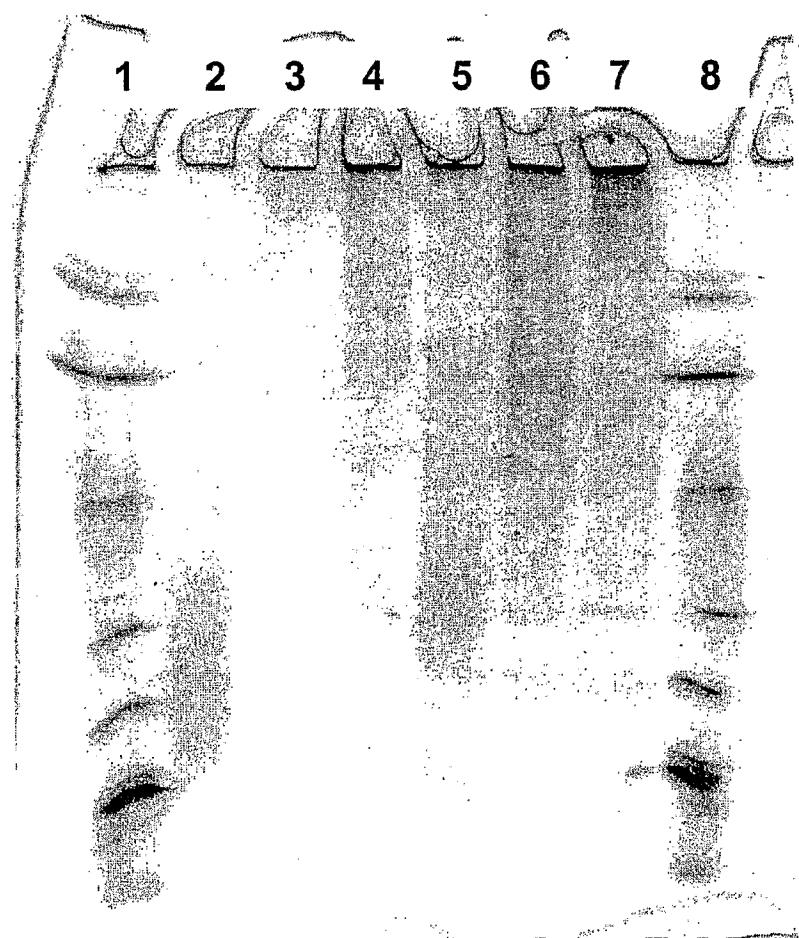


FIG. 164

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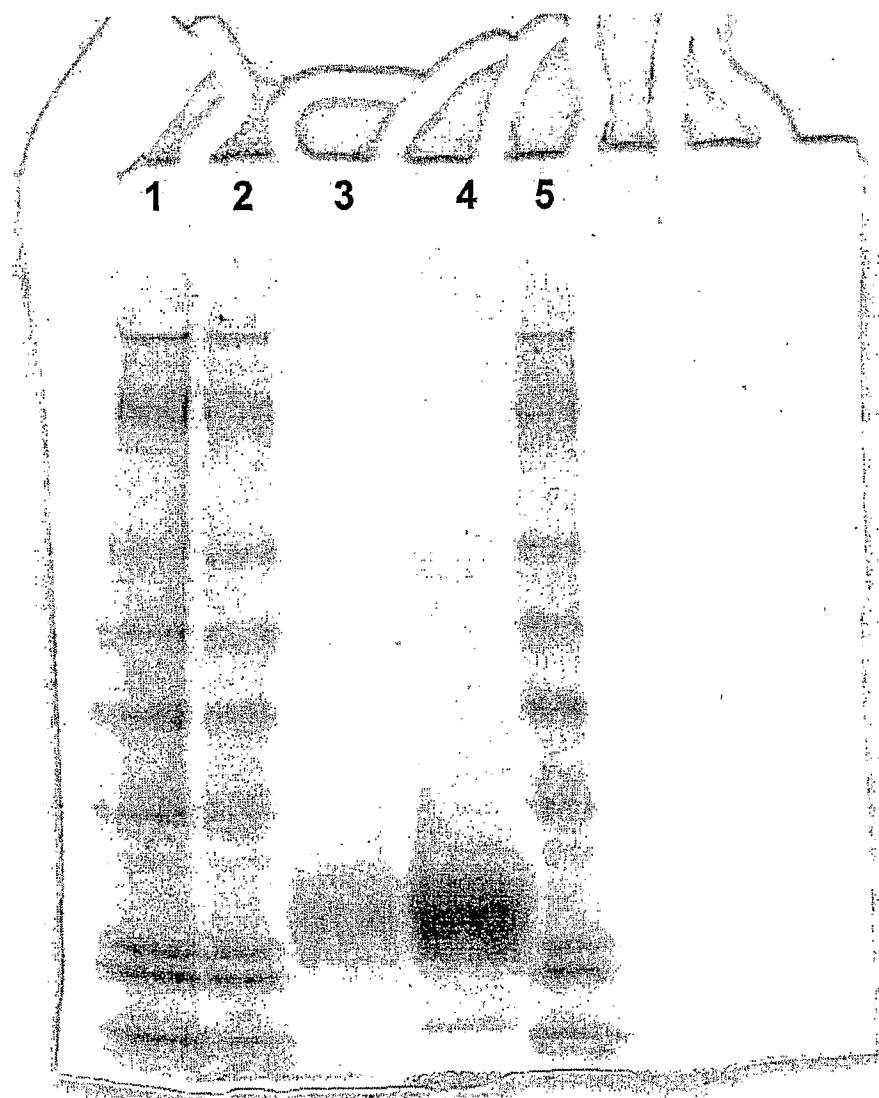


FIG. 165

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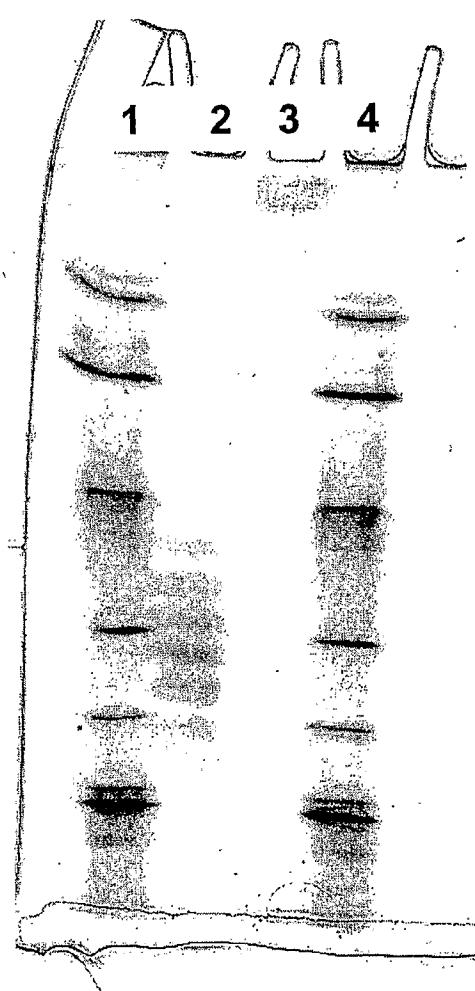


FIG. 166

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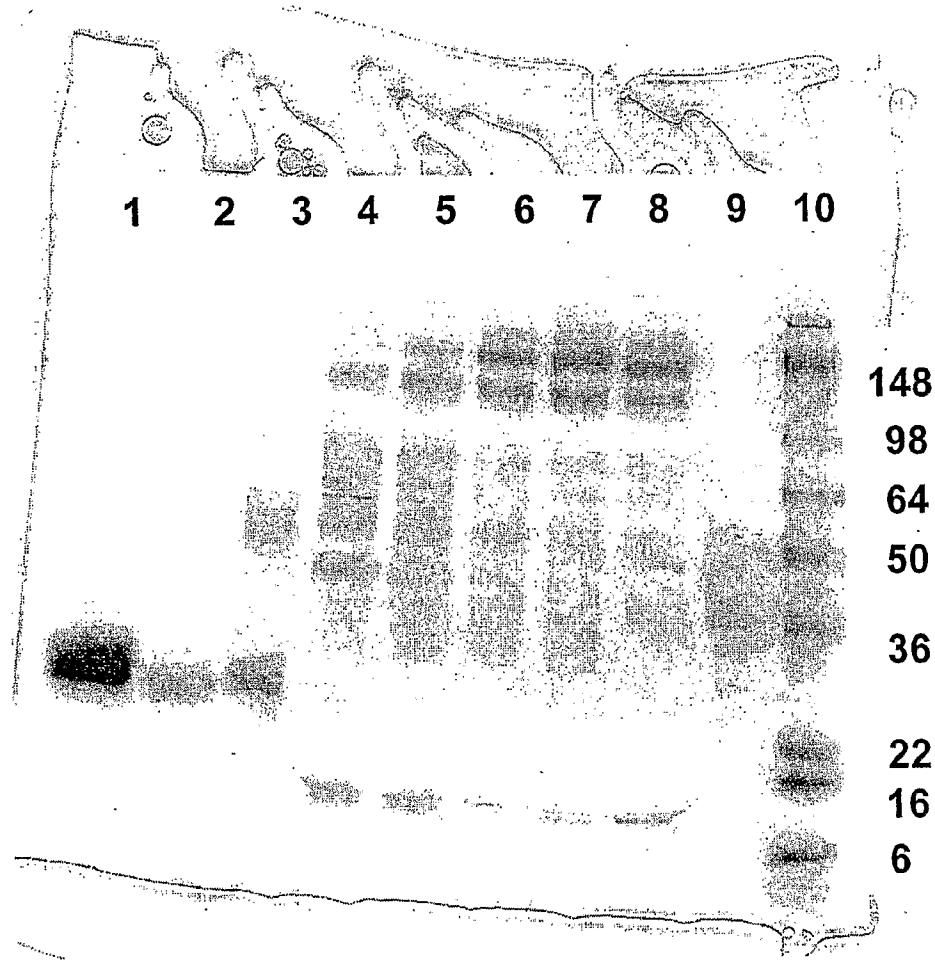


FIG. 167

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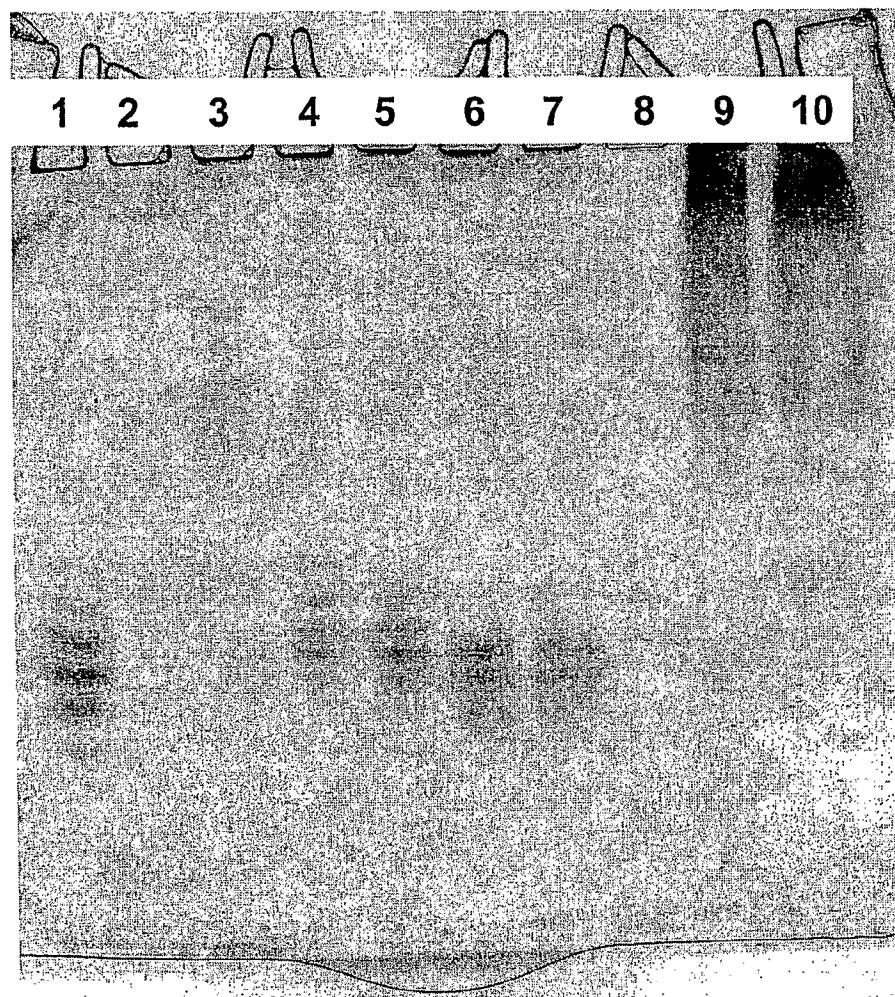


FIG. 168

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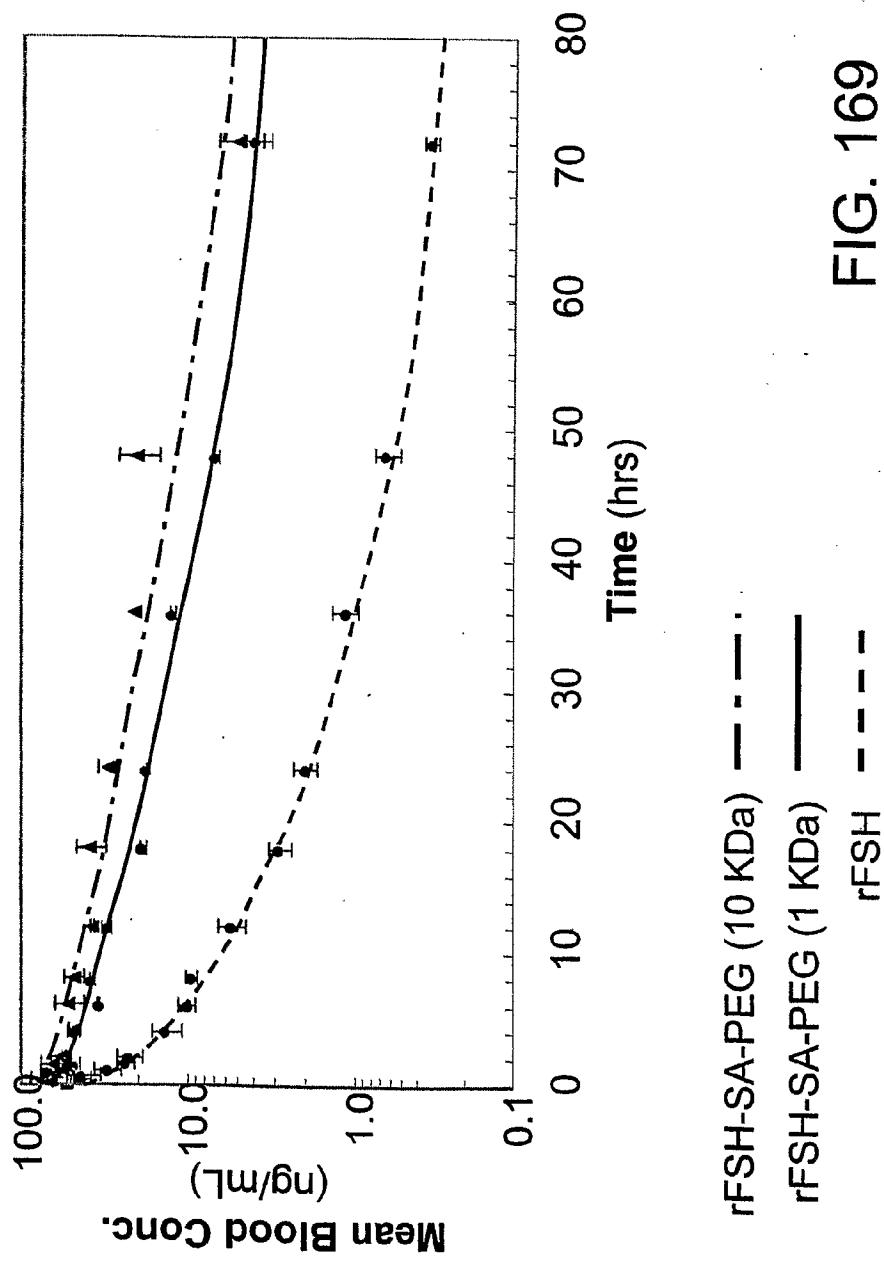


FIG. 169

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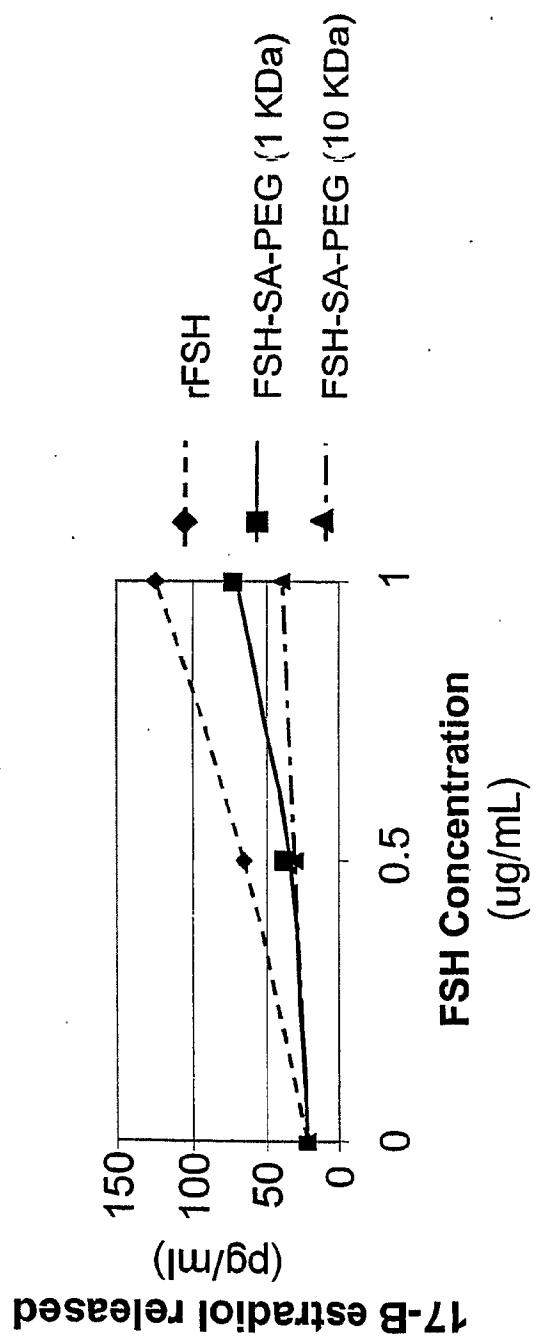


FIG. 170

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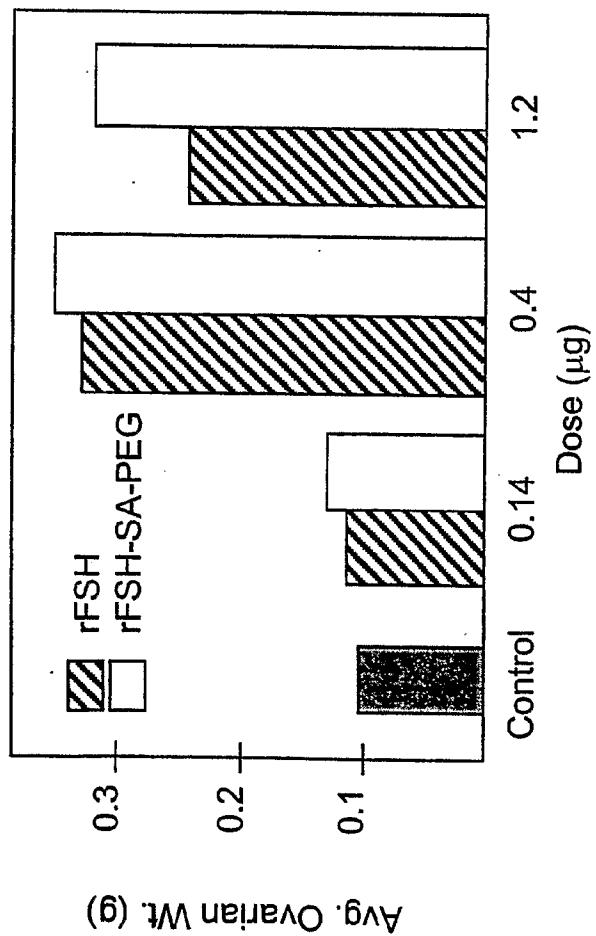


FIG. 171

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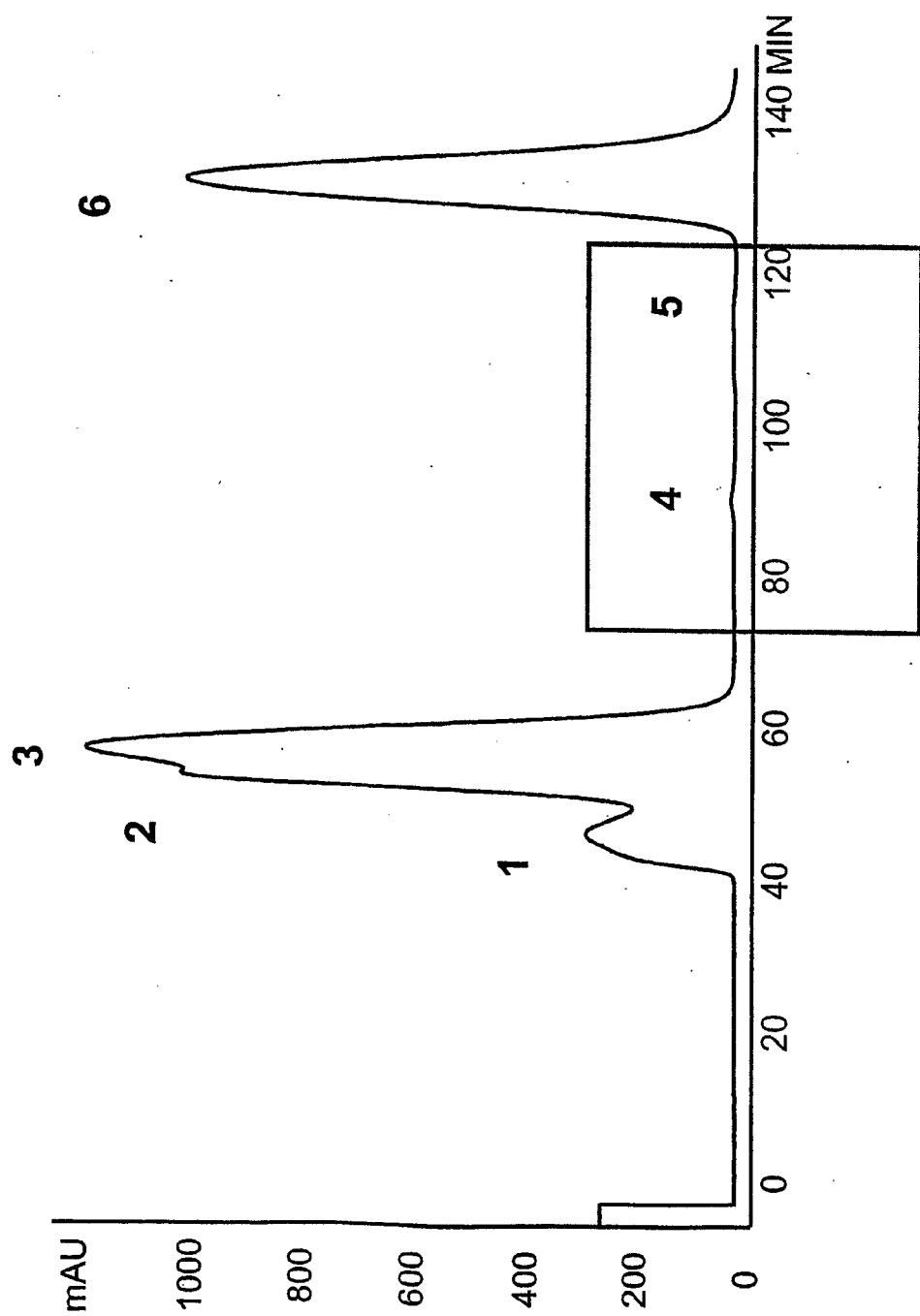


FIG. 172A

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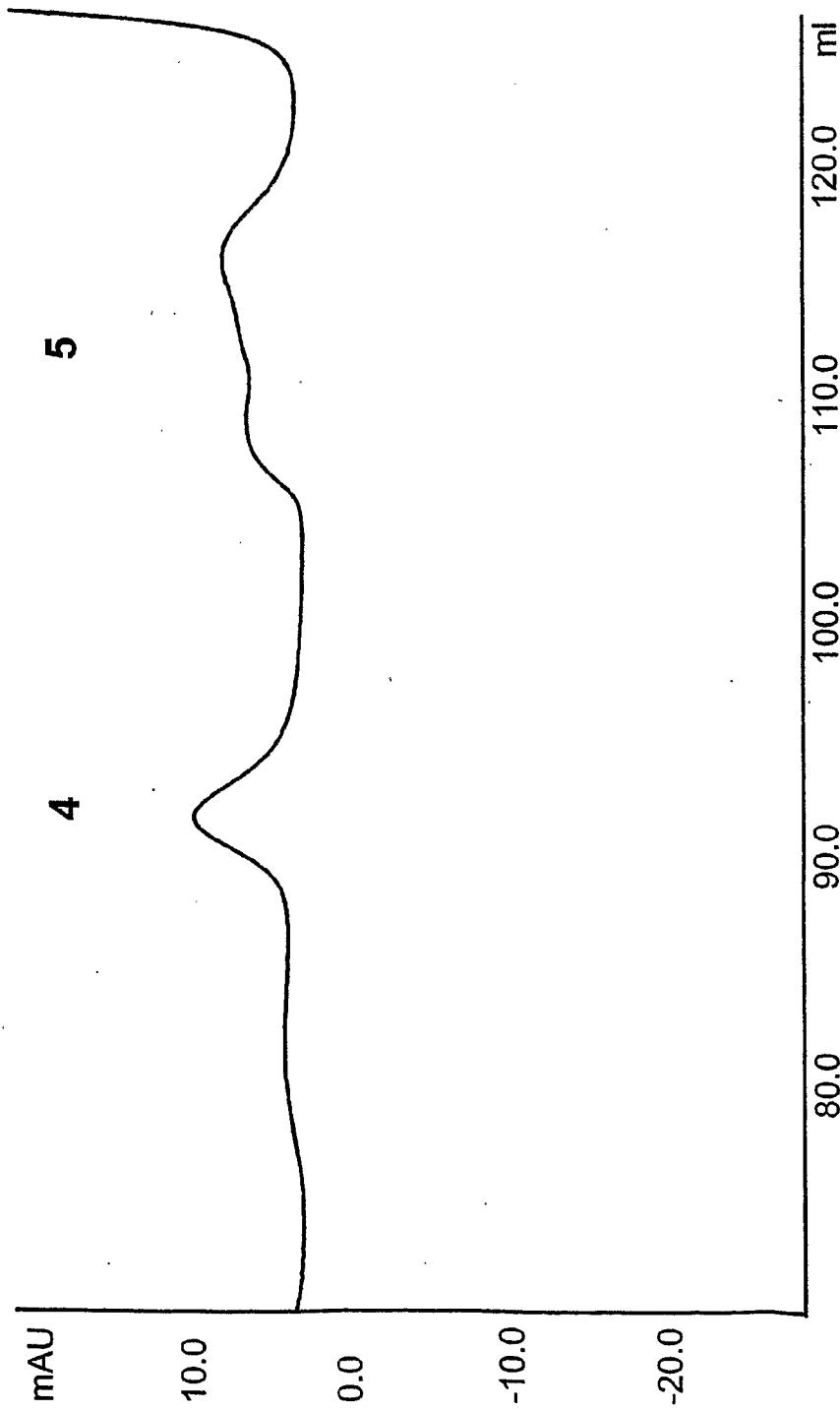


FIG. 172B

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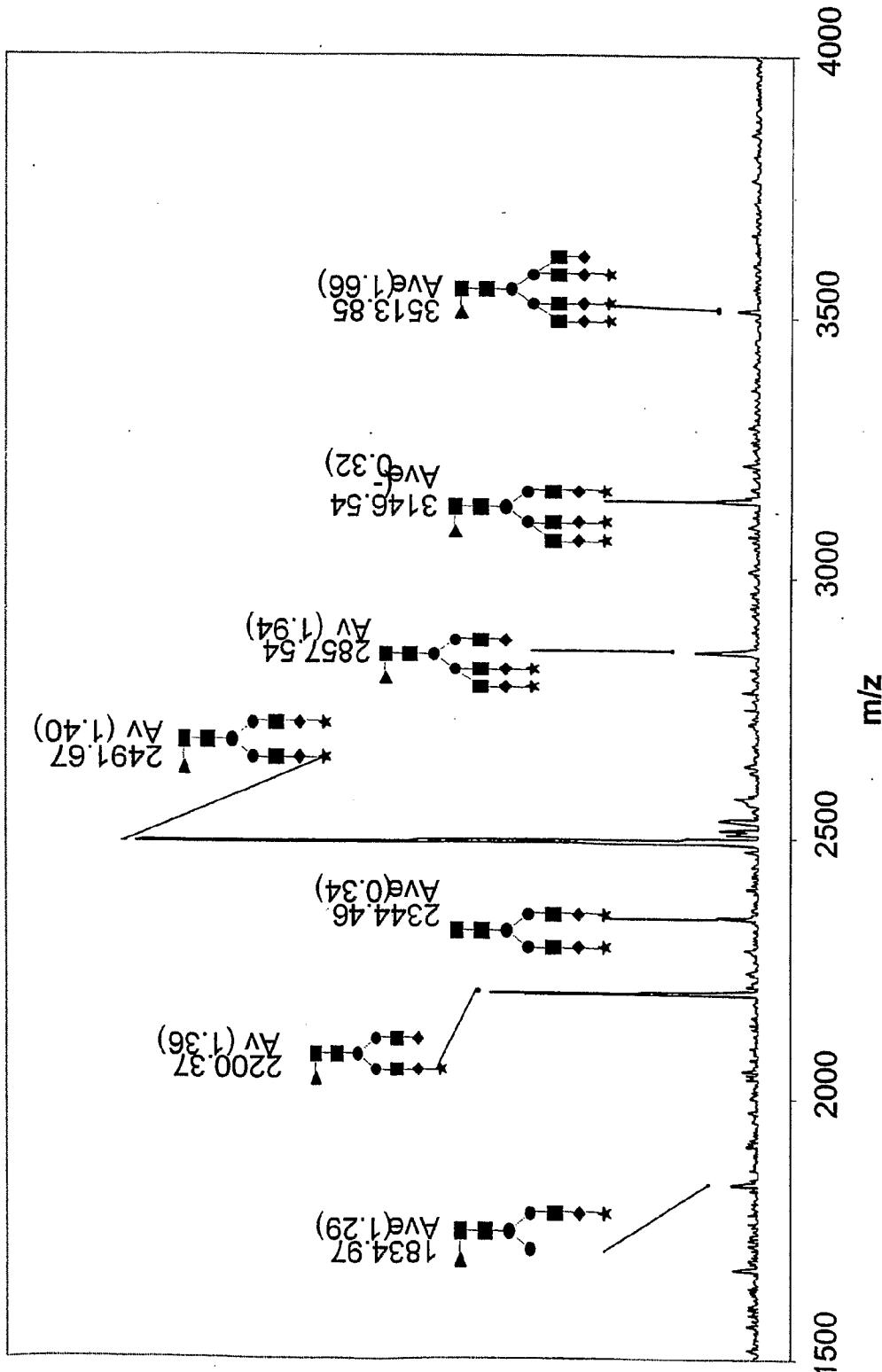


FIG. 173A

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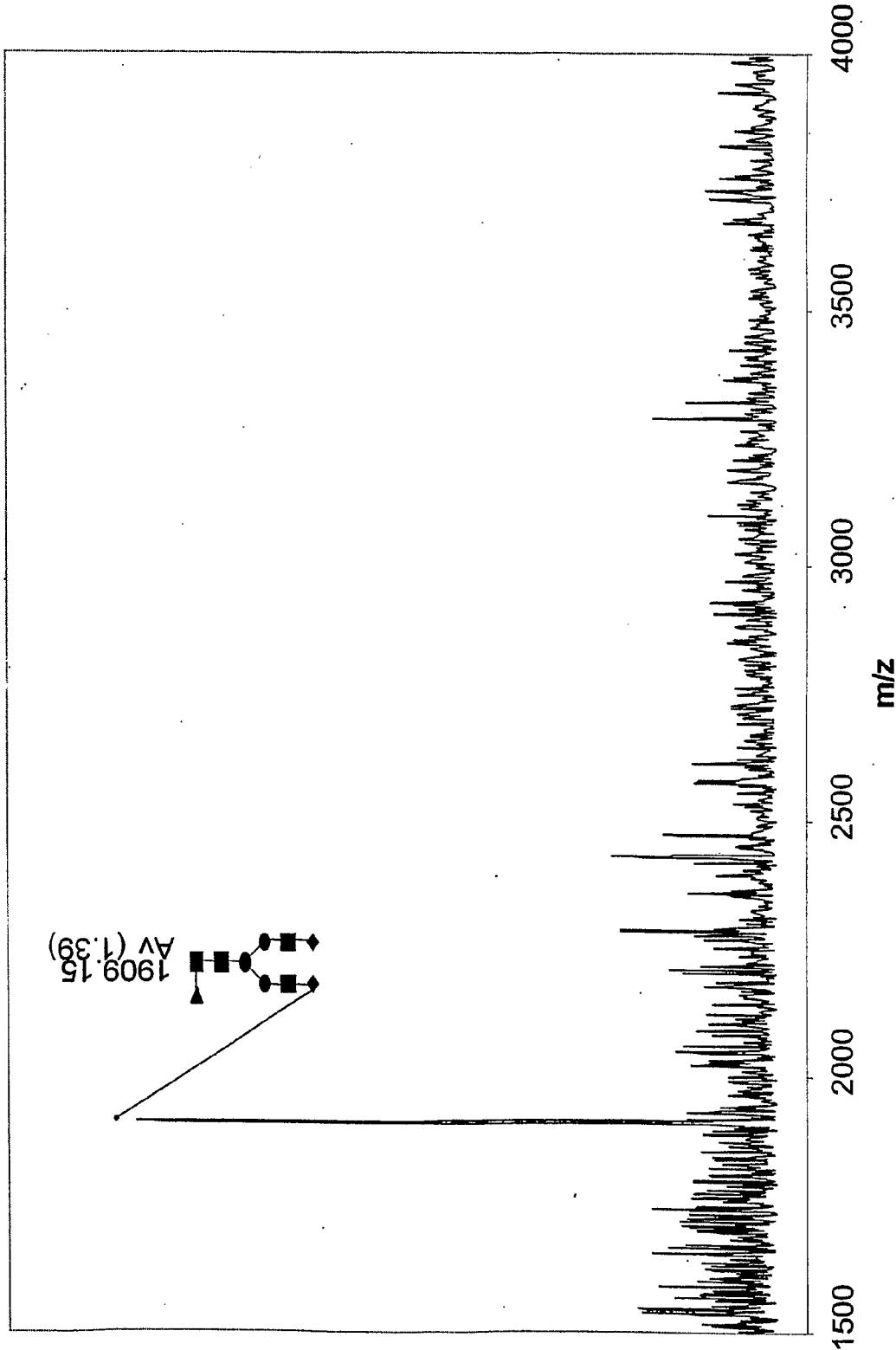


FIG. 173B

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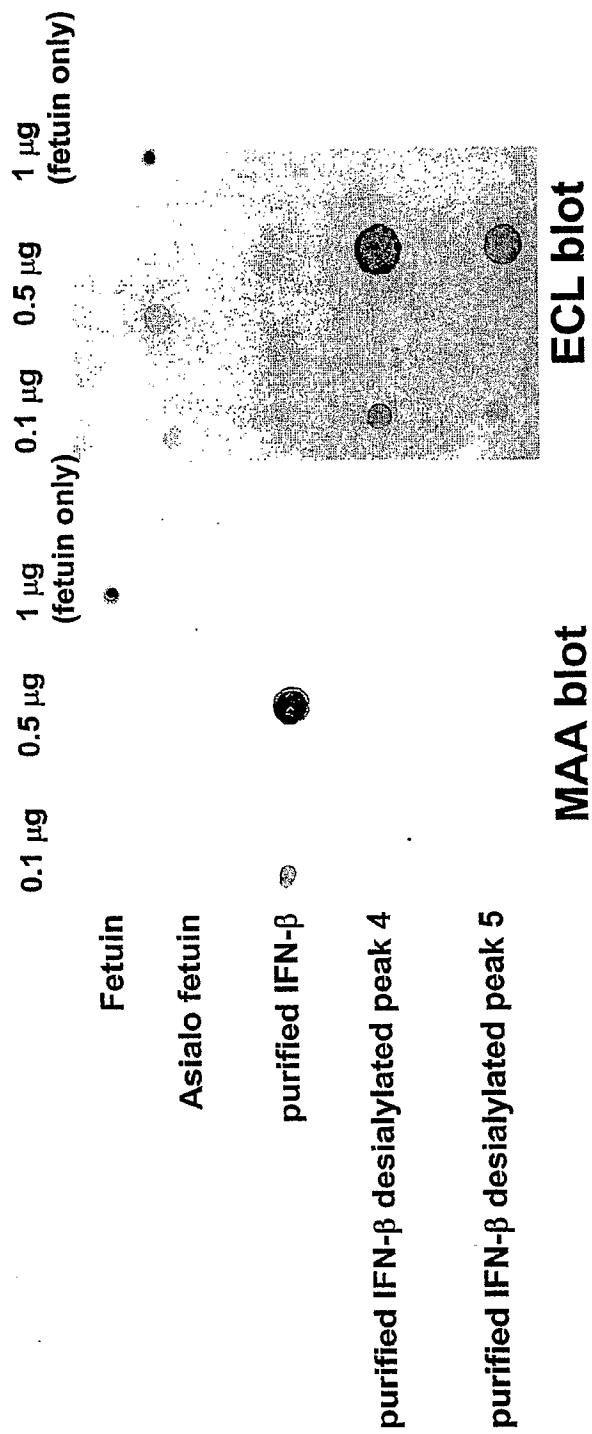


FIG. 174

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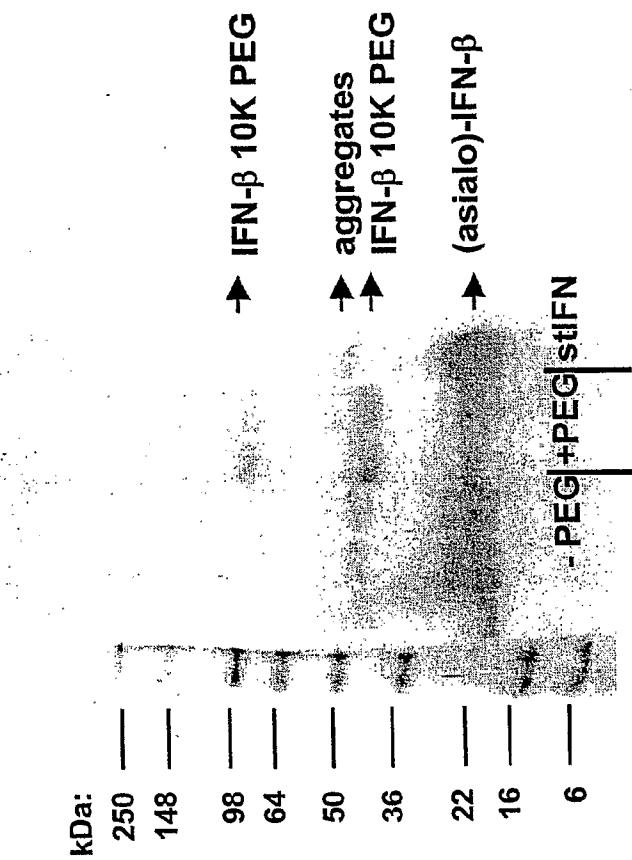
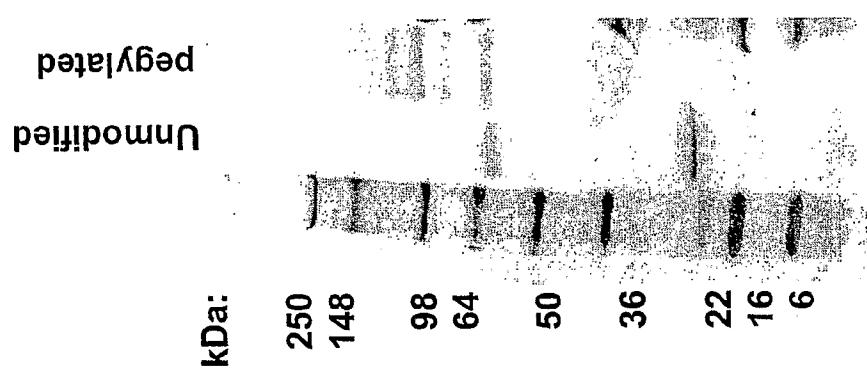


FIG. 175

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FIG. 176



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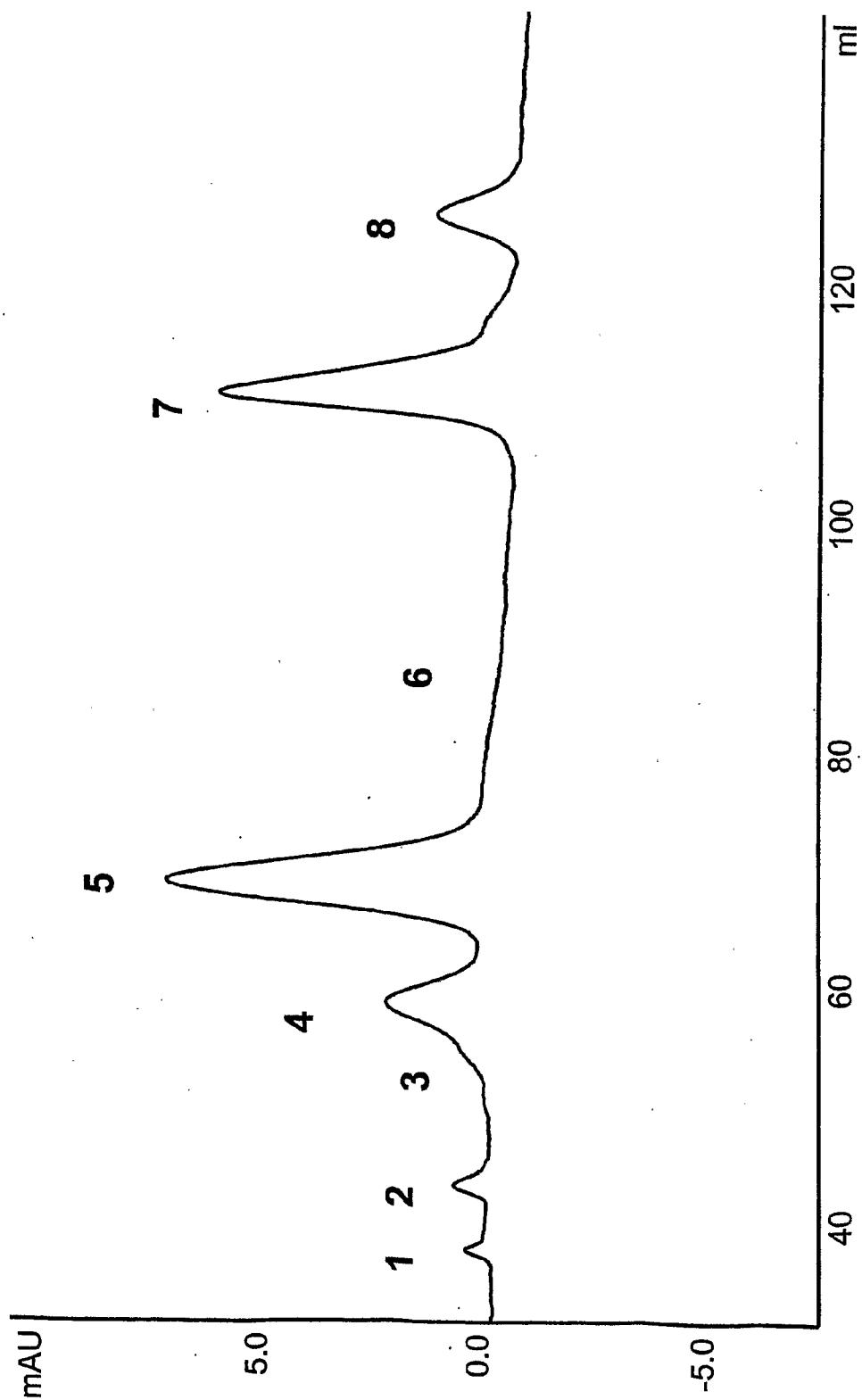


FIG. 177

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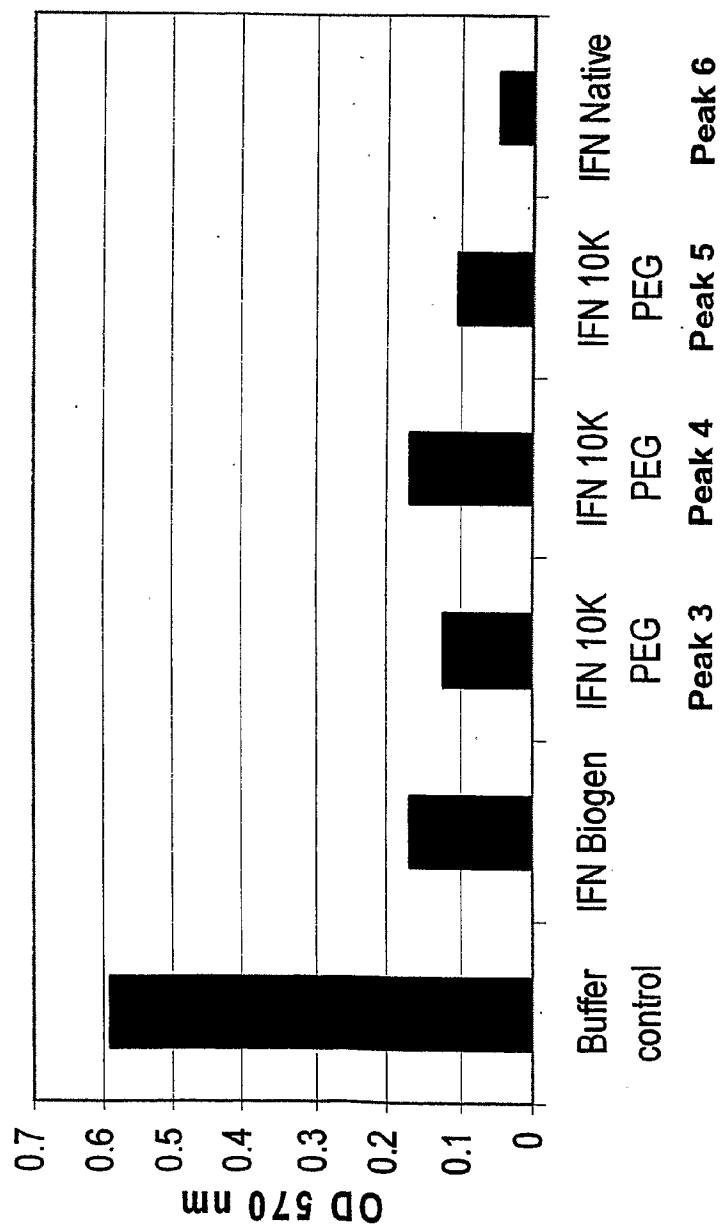


FIG. 178

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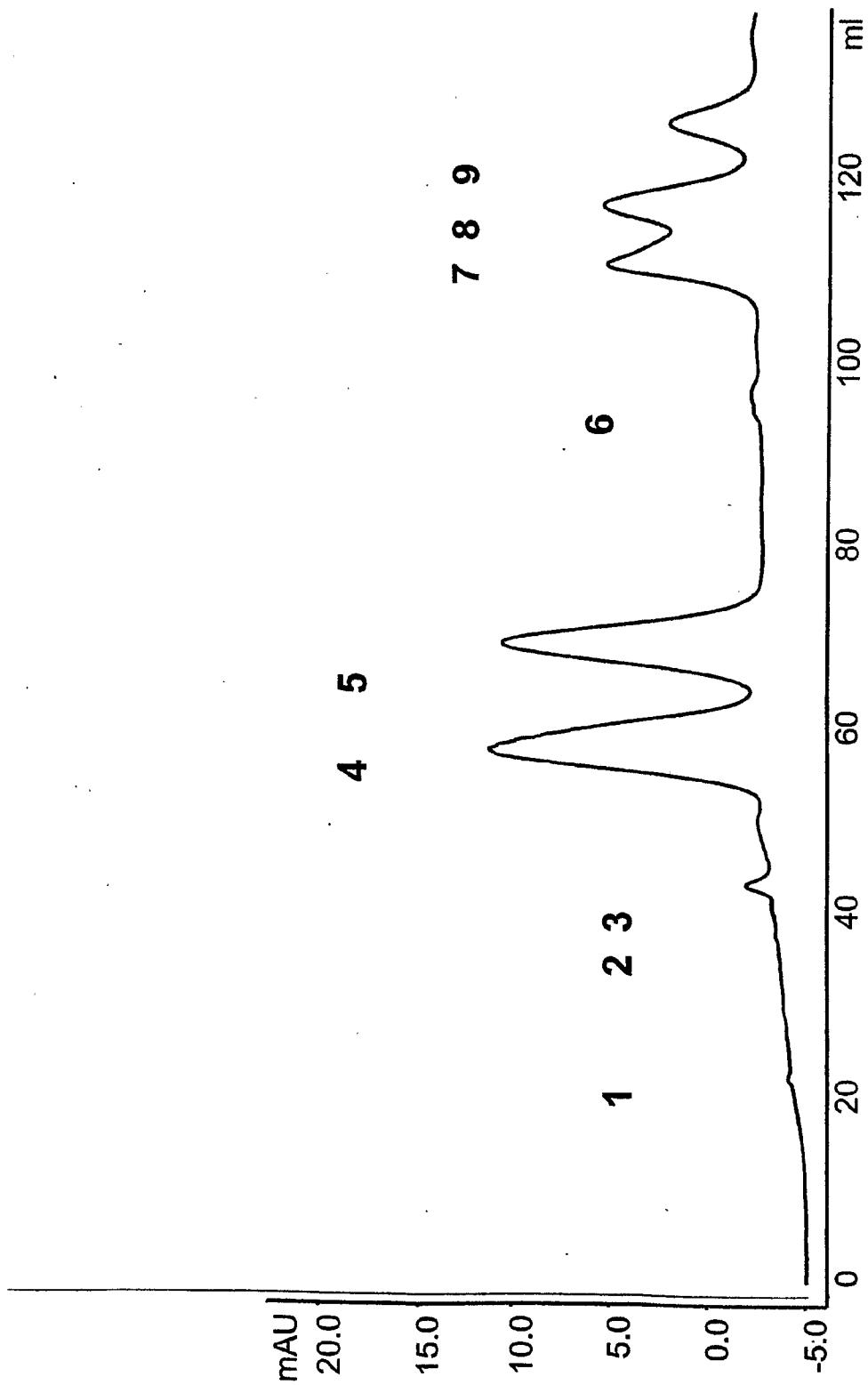


FIG. 179

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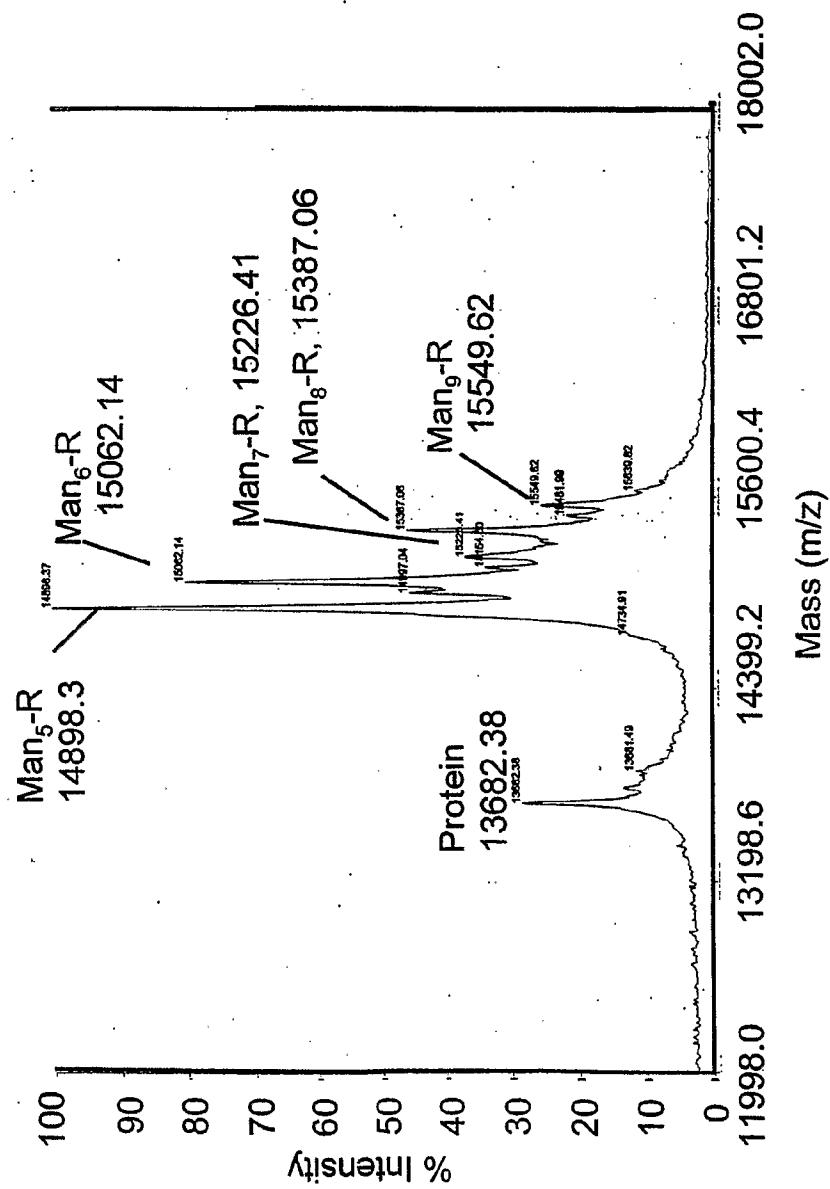


FIG. 180A

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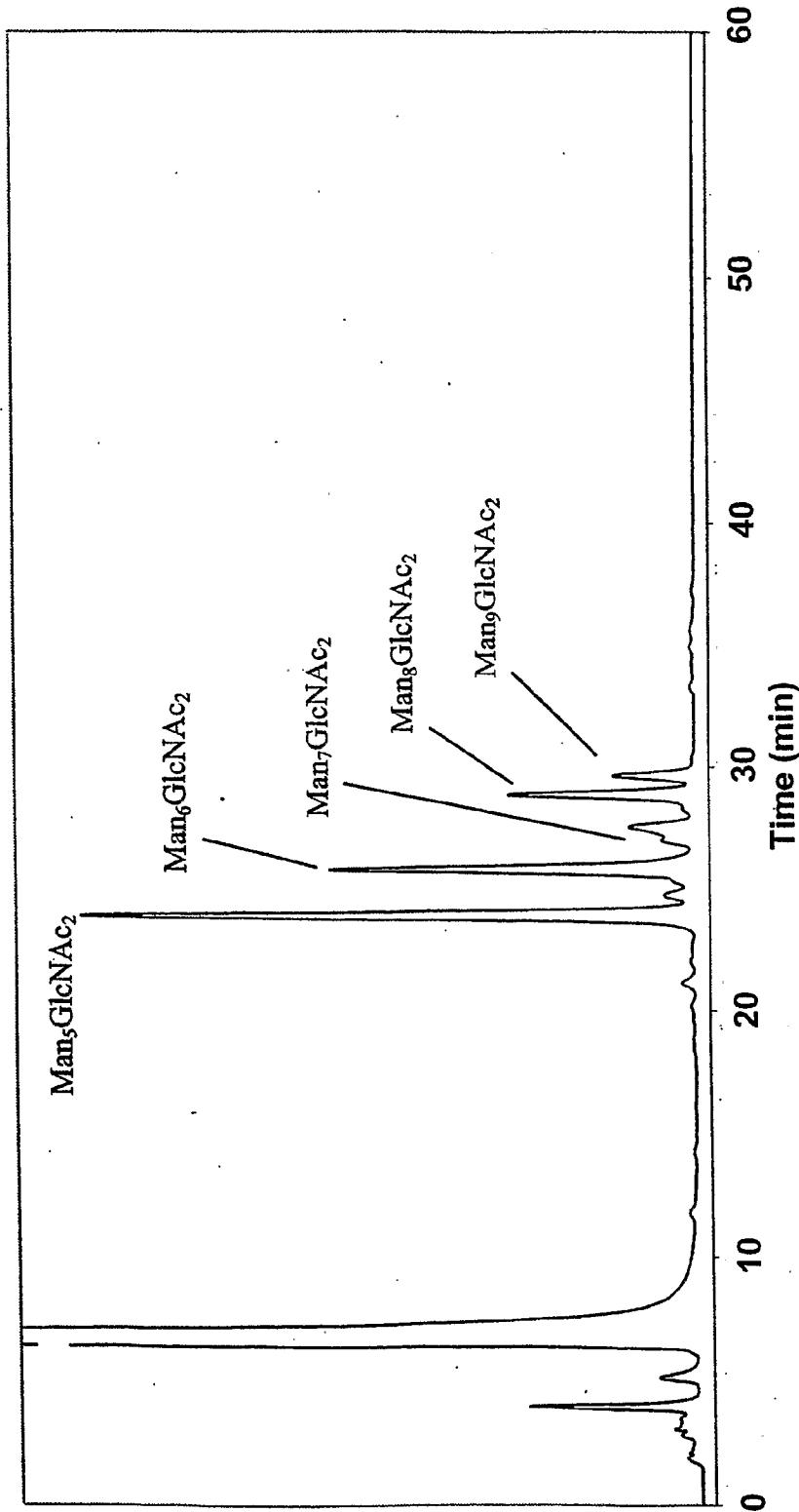


FIG. 180B

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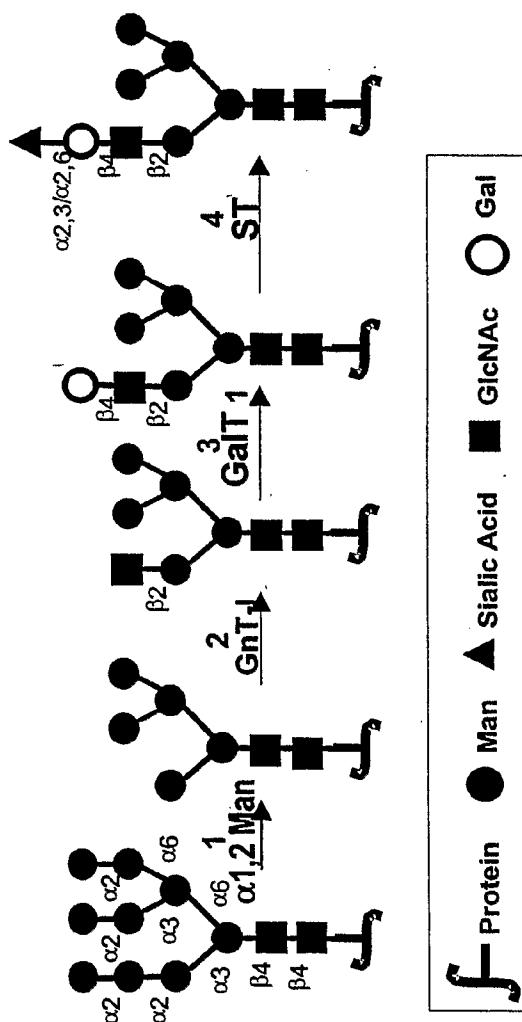


FIG. 181

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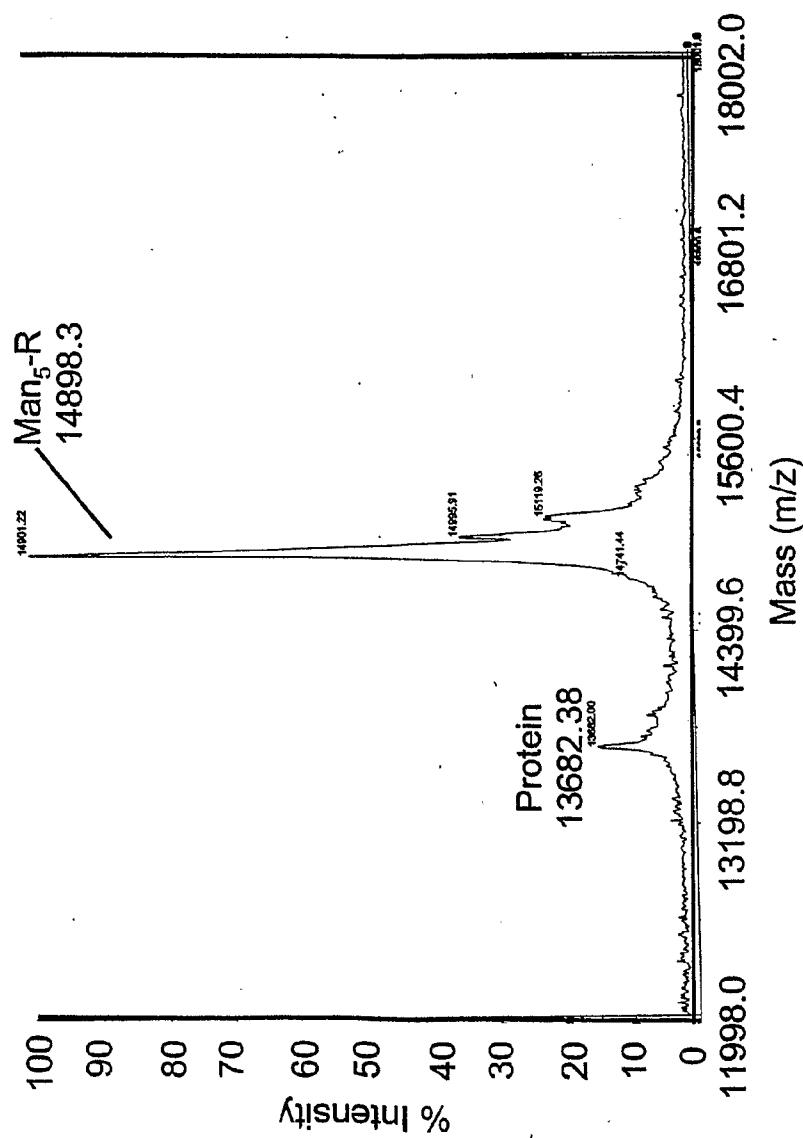


FIG. 182A

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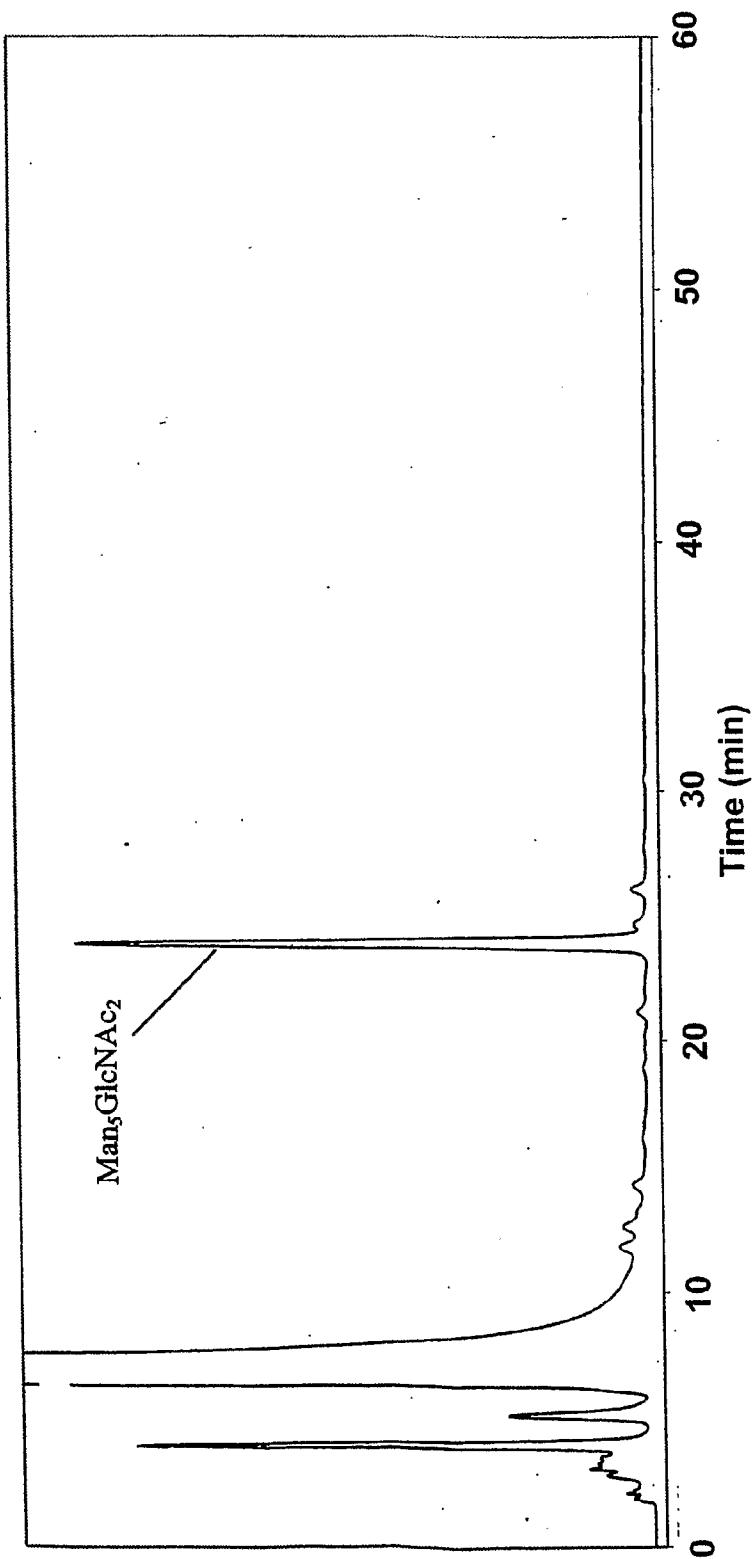


FIG. 182B

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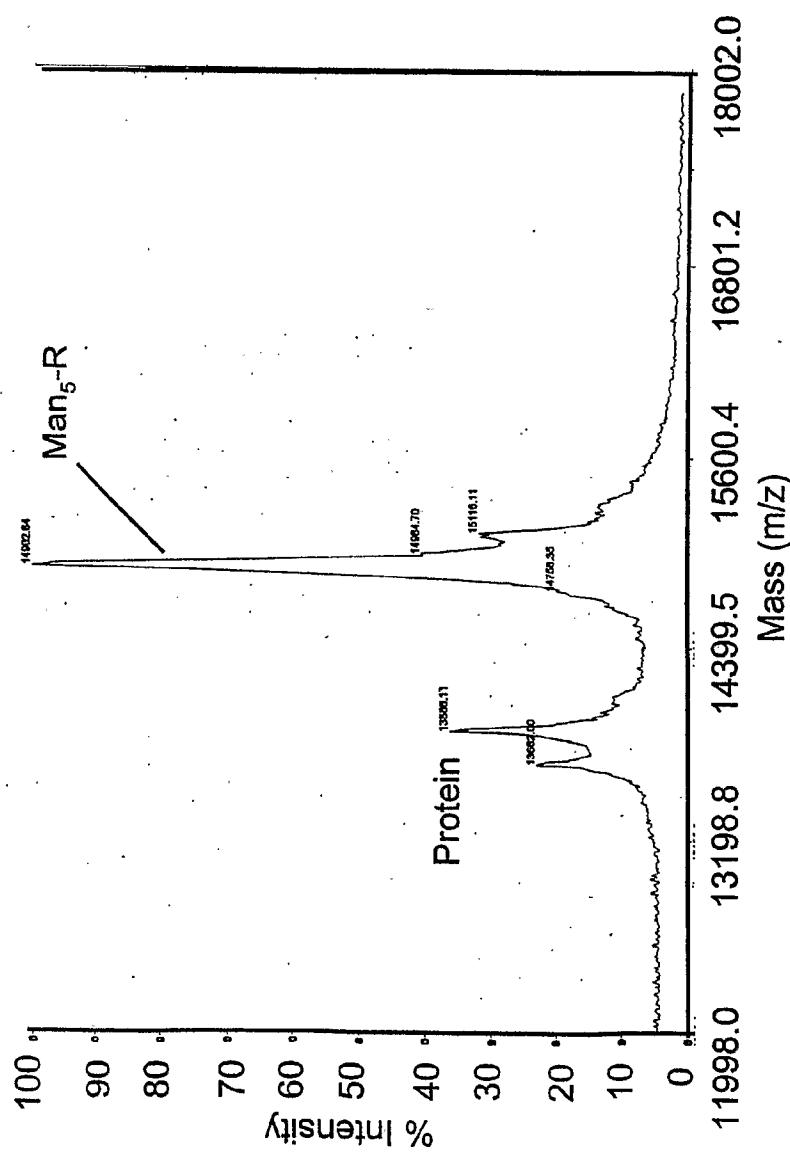


FIG. 183

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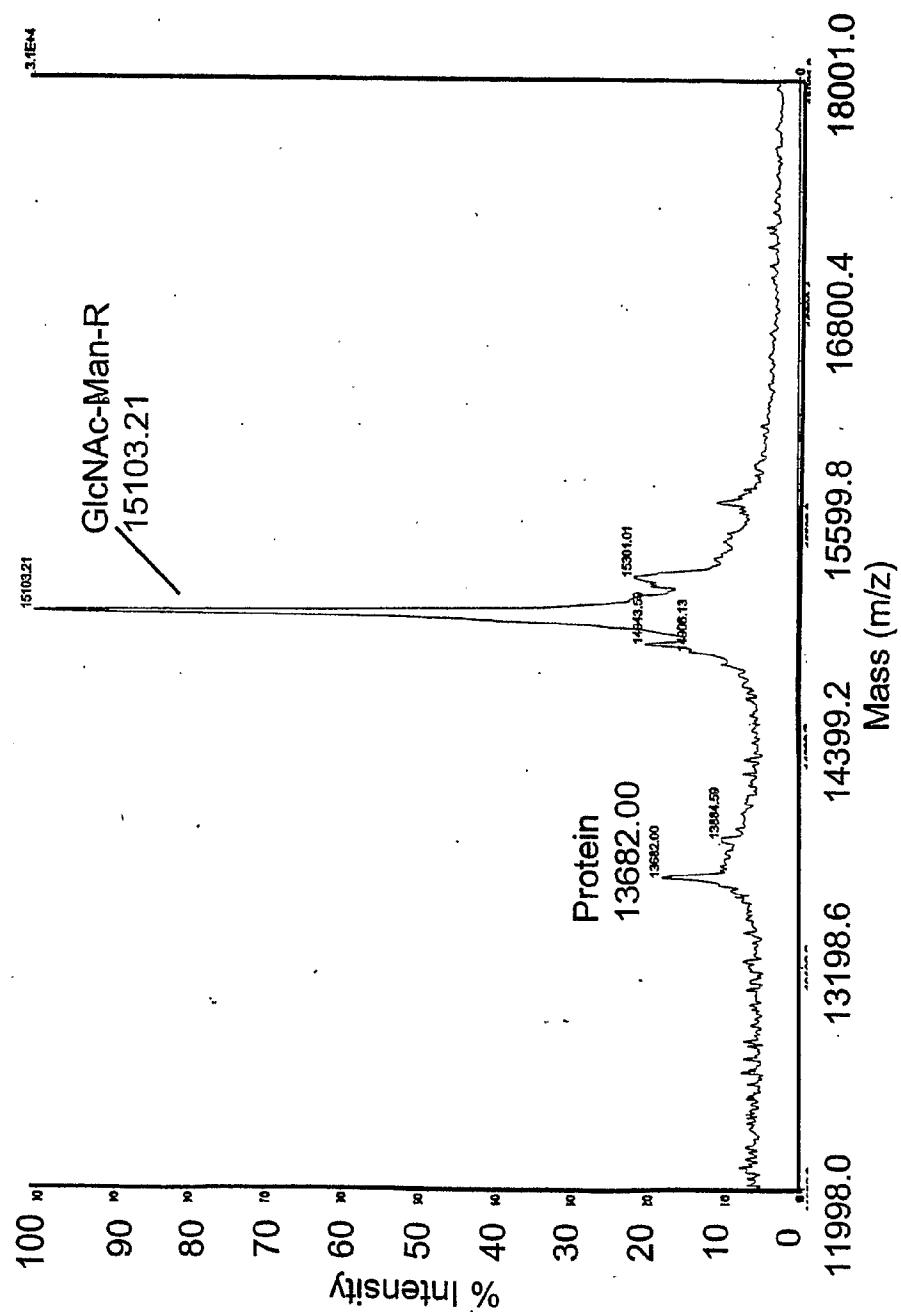


FIG. 184

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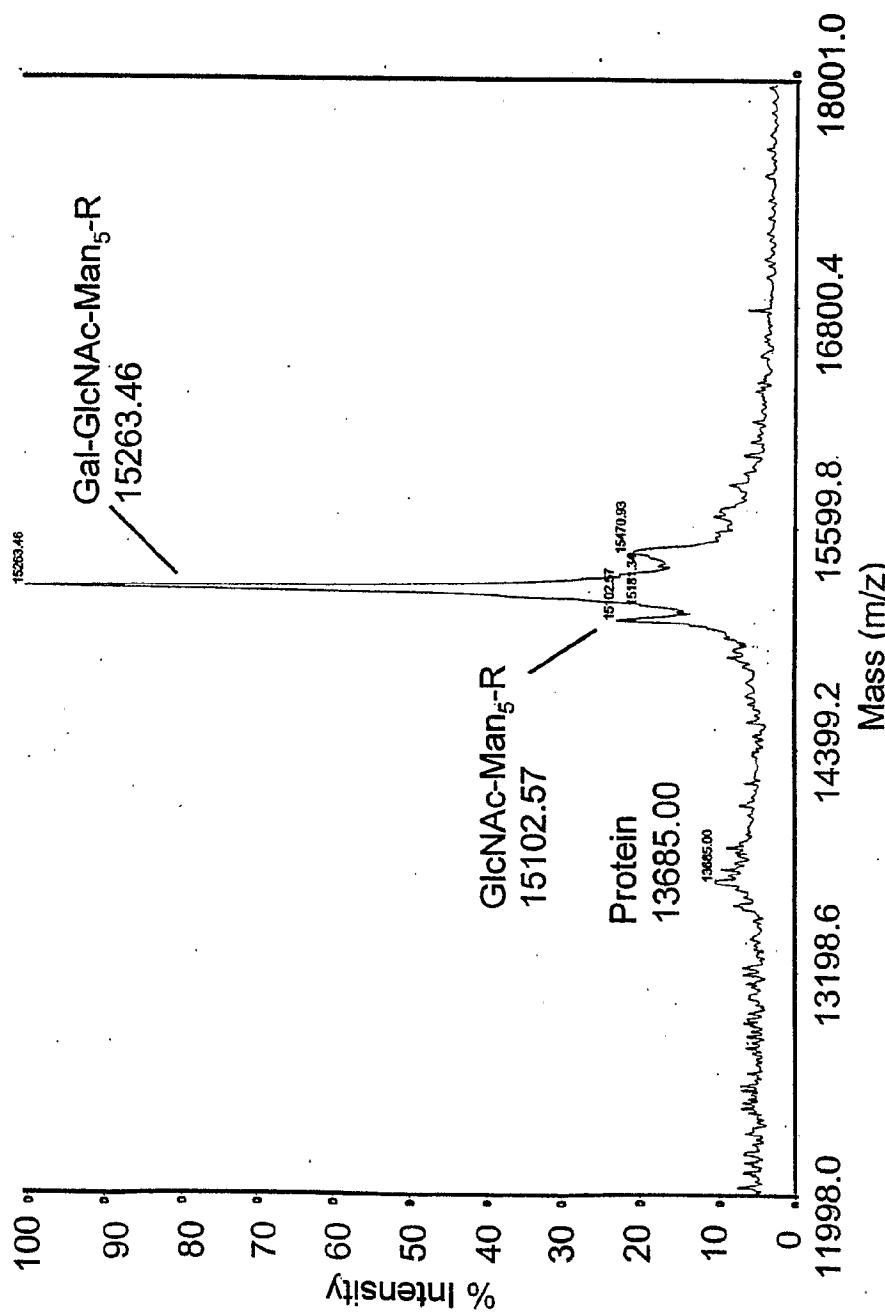


FIG. 185

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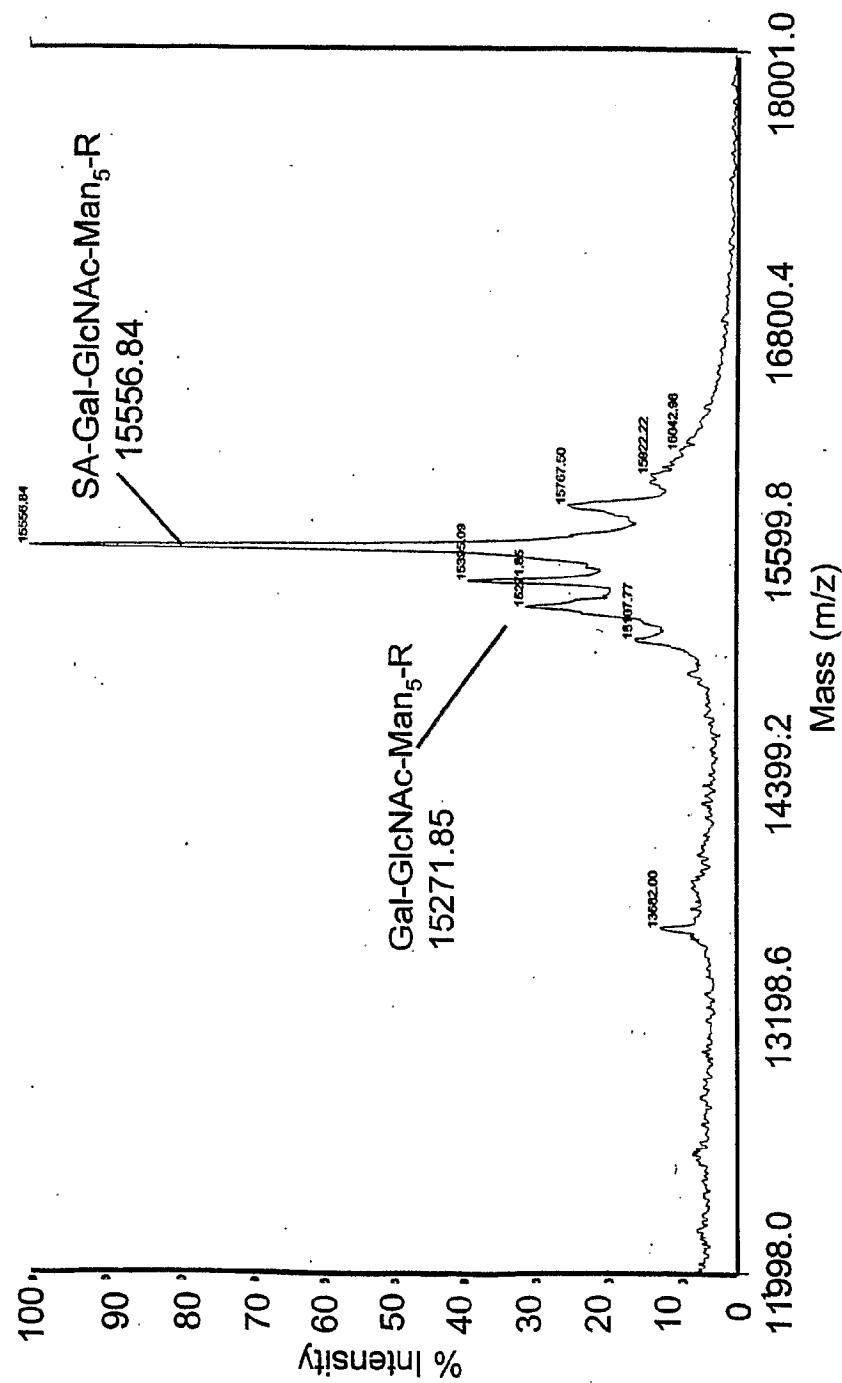


FIG. 186

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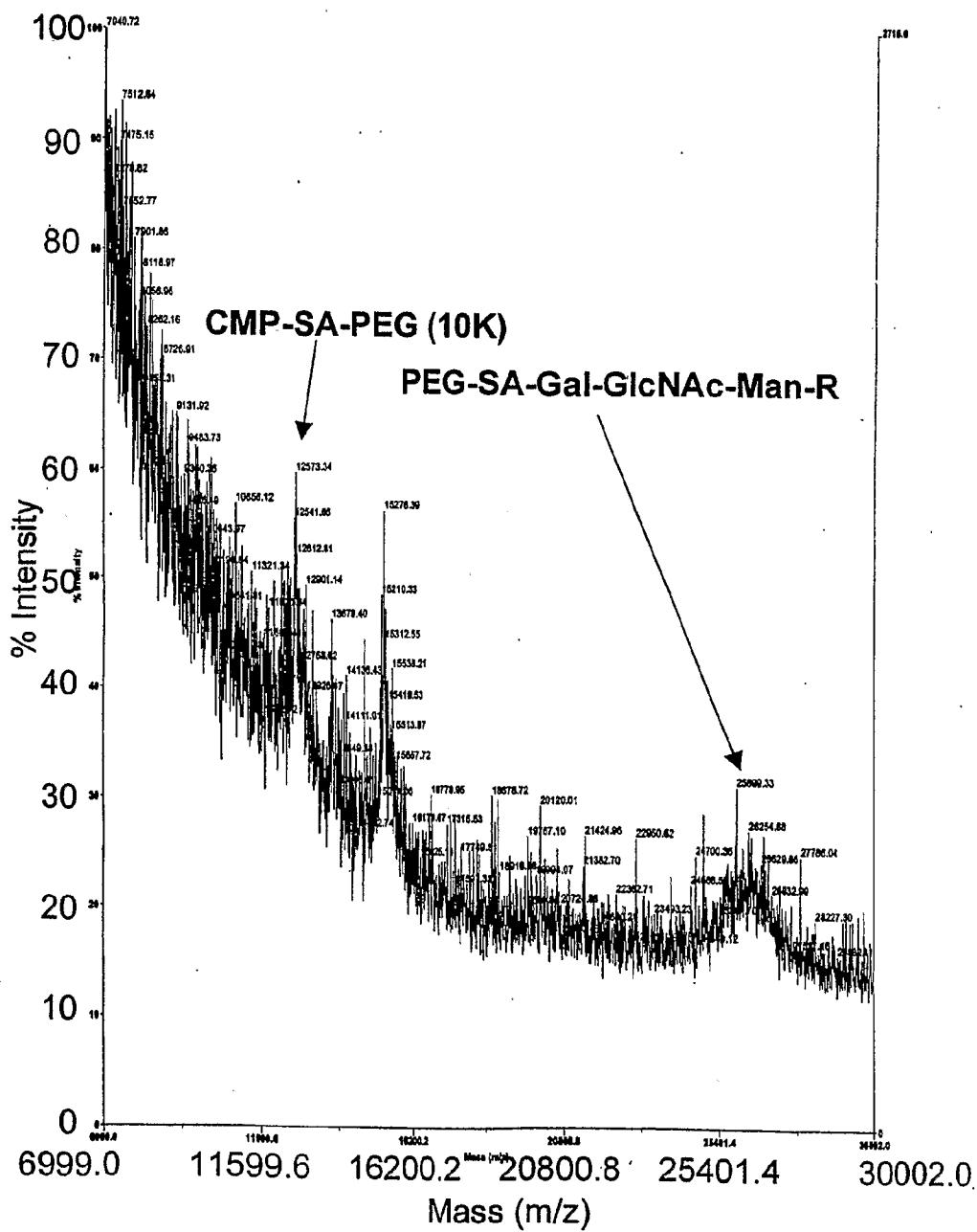


FIG. 187A

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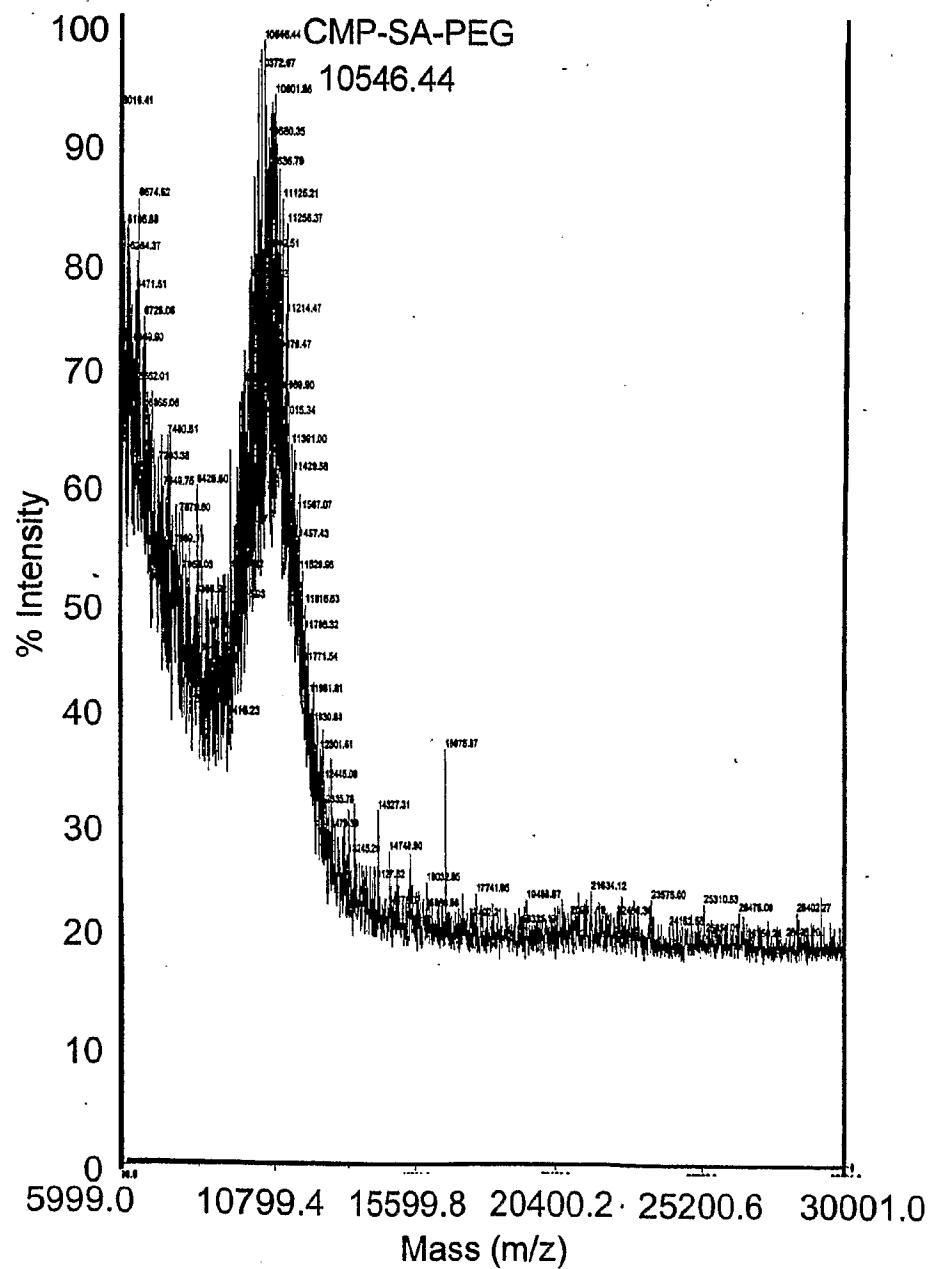
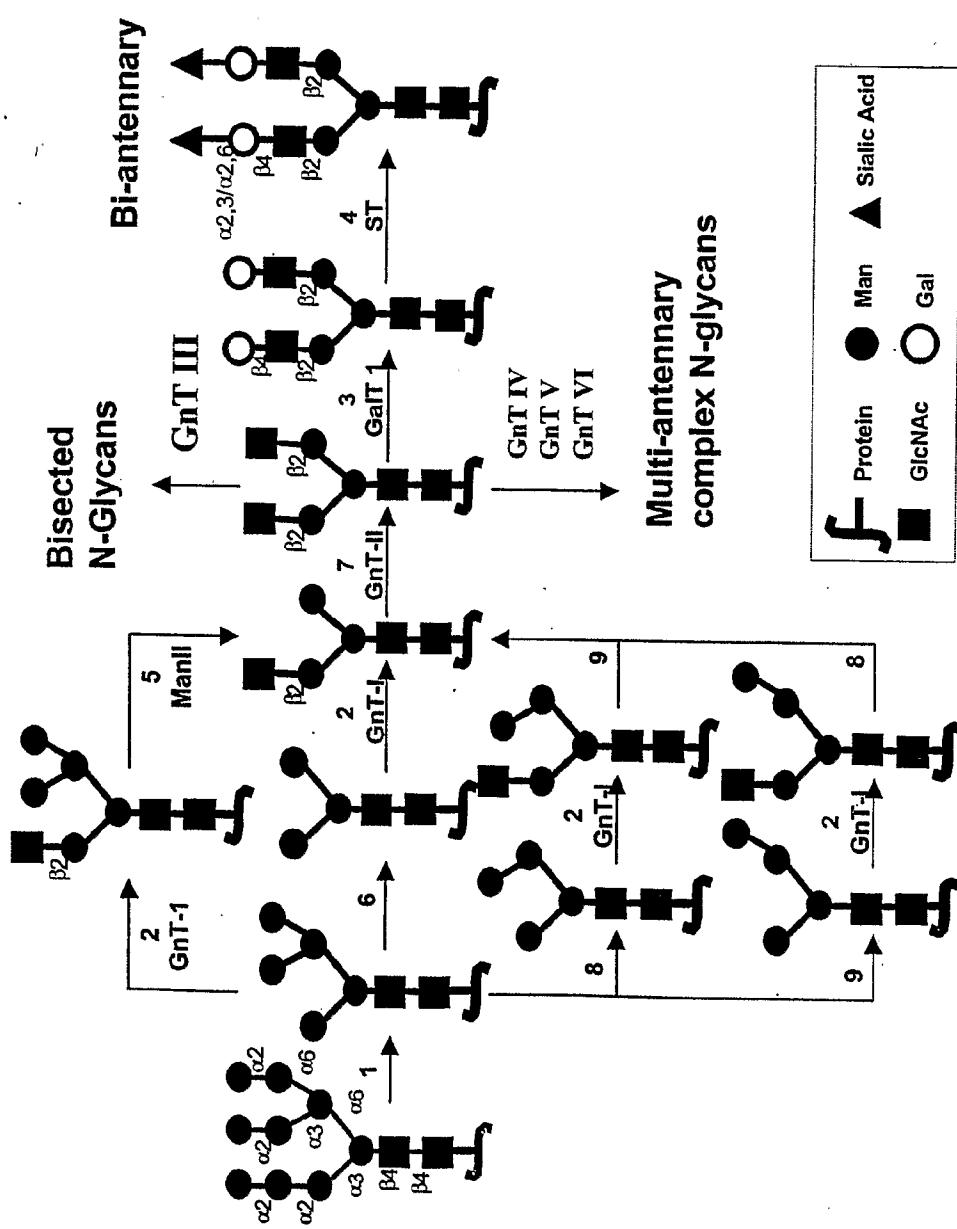


FIG. 187B

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FIG. 188



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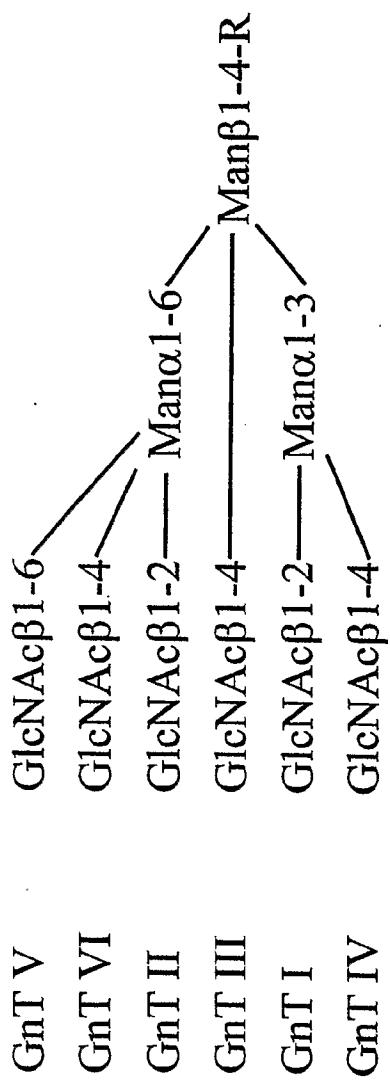


FIG. 189

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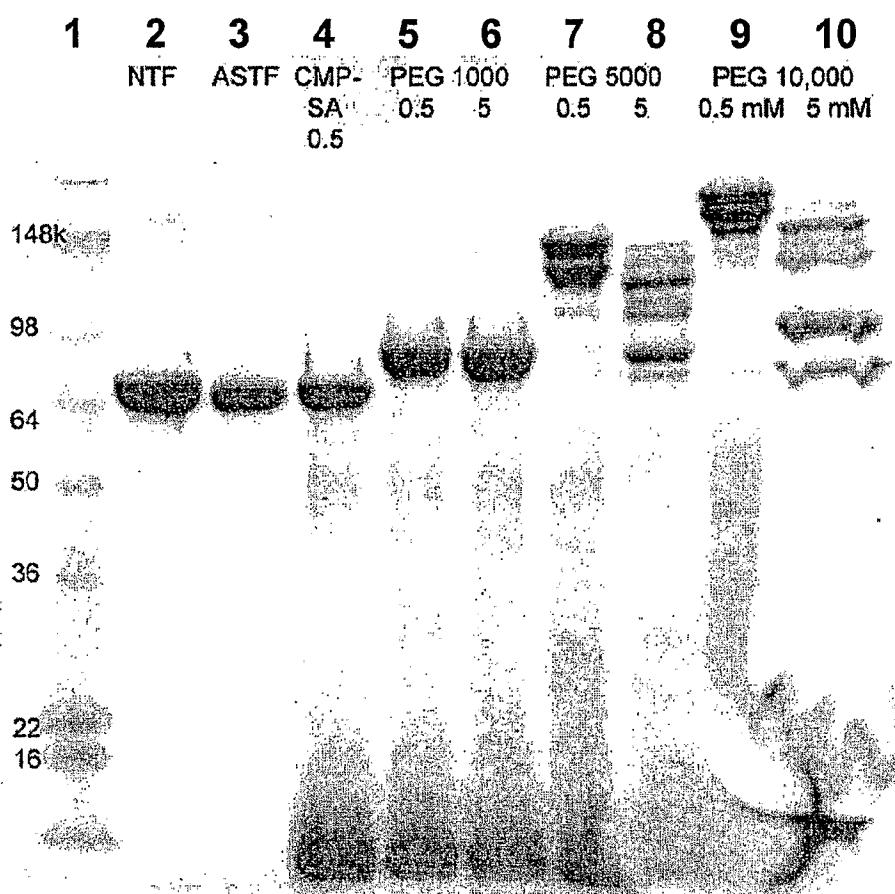


FIG. 190

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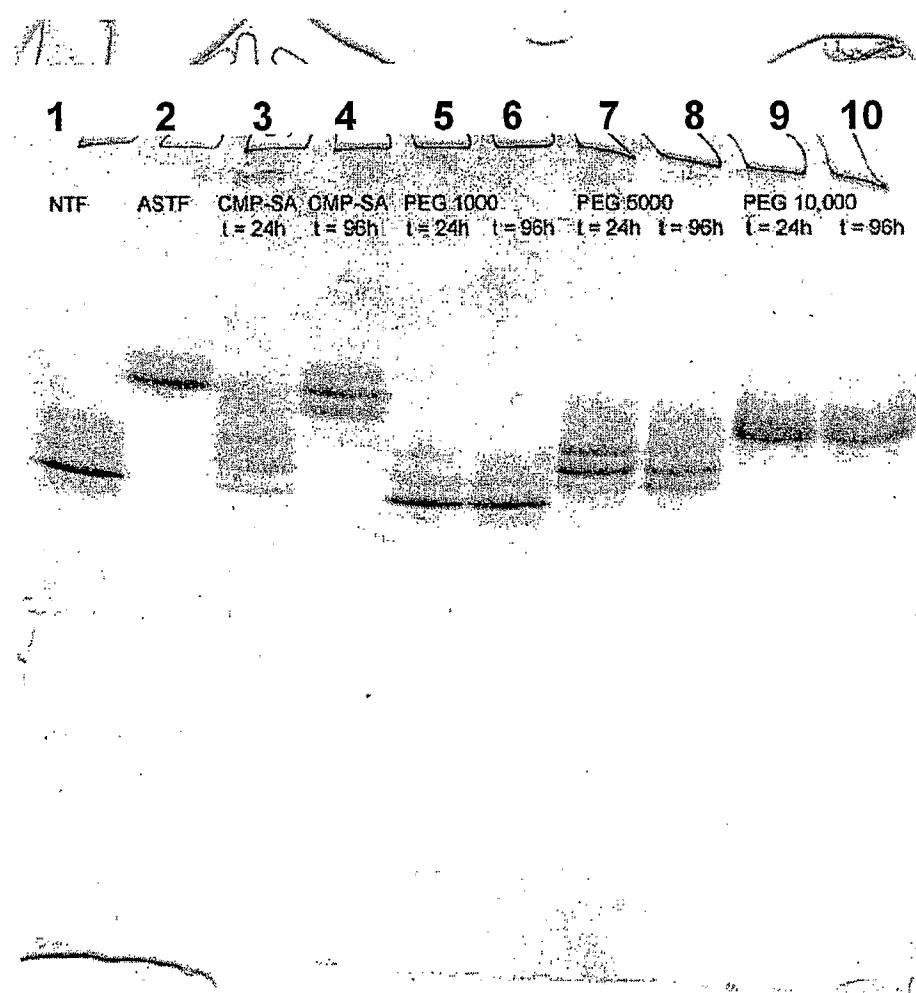
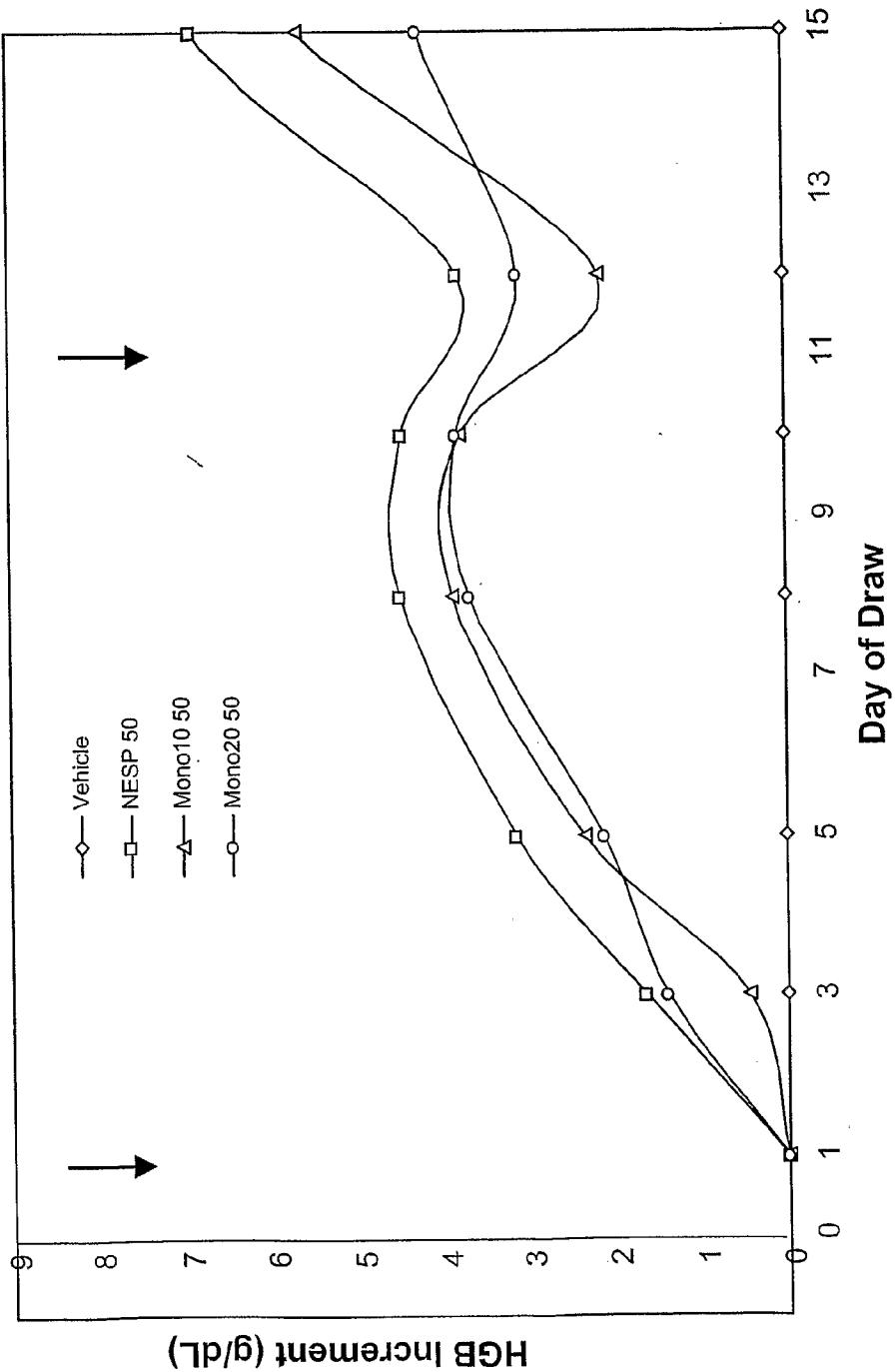


FIG. 191

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Fig. 192 Hemoglobin response in rats



SEQUENCE LISTING

<110> Neose Technologies, Inc.
DeFrees, Shawn
Zopf, David
Bayer, Robert
Hakes, David
Chen, Xi
Bowe, Caryne

<120> ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF ERYTHROPOIETIN

<130> 040853-01-5083WO

<150> PCT/US02/32263
<151> 2002-10-09

<150> US 10/287,994
<151> 2002-11-5

<150> US 10/360,770
<151> 2003-01-06

<150> US 10/369,779
<151> 2003-03-17

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gcctctgctt tccagcgcccg ggcaggagggg gtcctgggttg cctcccatctt gcagagcttc 480
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<210> 2
<211> 174
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Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
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Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170

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tgcaataata aaacattaac tttatacttt ttaatttaat gtatagaata gagatataca 180

taggatatgt aaatagatac acagtgtata tgtgattaaa atataatggg agattcaatc 240

agaaaaaaagt ttctaaaaag gctctgggt aaaagaggaa ggaaacaata atgaaaaaaa 300

tgtggtgaga aaaacagctg aaaacccatg taaagagtgt ataaagaaag caaaaagaga 360

agttagaaagt aacacagggg catttggaaa atgttaacga gtatgtccc tatttaaggc 420

taggcacaaa gcaaggctt cagagaacct ggagcctaag gtttaggctc acccattca 480

accagtctag cagcatctgc aacatctaca atggccttga cctttgttt actggtgcc 540

ctcctggtgc tcaagctgcaa gtcaagctgc tctgtggct gtgatctgcc tcaaaccac 600

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agcacaaagg	actcatctgc	tgcttggat	gagaccctcc	tagacaaatt	ctacactgaa	840
ctctaccagc	agctgaatga	cctggaagcc	tgtgtgatac	agggggtggg	ggtgacagag	900
actcccctga	tgaaggagga	ctccattctg	gctgtgagga	aatacttcca	aagaatcact	960
ctctatctga	aagagaagaa	atacagccct	tgtgcctggg	aggttgcag	agcagaaatc	1020
atgagatctt	tttctttgtc	aacaaacttg	caagaaagtt	taagaagtaa	ggaatgaaaa	1080
ctgggtcaac	atggaaatga	tttcattga	ttcgtatgcc	agctcacctt	tttatgatct	1140
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ctgattacag	aataactggt	acacttcatt	tgtccatcaa	tattatattc	aagatataag	1560
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aacaaataaca	attctgctct	cttgtgtatt	tgattttgt	atgaaaaaaaaa	ctaaaaatgg	1680
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<211> 188

<212> PRT

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Lys	Ser	Ser	Cys	Ser	Val	Gly	Cys	Asp	Leu	Pro	Gln	Thr	His	Ser	Leu
															30
20															

Gly	Ser	Arg	Arg	Thr	Leu	Met	Leu	Leu	Ala	Gln	Met	Arg	Arg	Ile	Ser
35															

Leu	Phe	Ser	Cys	Leu	Lys	Asp	Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glu
50															

Glu	Phe	Gly	Asn	Gln	Phe	Gln	Lys	Ala	Glu	Thr	Ile	Pro	Val	Leu	His
65															

Glu	Met	Ile	Gln	Gln	Ile	Phe	Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser

85

90

95

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
 100 105 110

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
 115 120 125

Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
 130 135 140

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
 165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
 180 185

<210> 5

<211> 757

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ctcctgtggc aattgaatgg gaggcttgaa tattgcctca aggacaggat gaactttgac 180

atccctgagg agattaagca gctgcagcag ttccagaagg aggacgccgc attgaccatc 240

tatgagatgc tccagaacat ctttgcttatt ttcagacaag attcatctag cactggctgg 300

aatgagacta ttgttgagaa ctcctggct aatgtctatc atcagataaa ccatctgaag 360

acagtcctgg aagaaaaact ggagaaagaa gatttacca ggggaaaact catgagcagt 420

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<210> 6

<211> 187

<212> PRT

<213> Homo sapiens

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 1 5 10 15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
 20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
 145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
 165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 180 185

<210> 7

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<212> DNA

<213> Homo sapiens

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 gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc 180
 tccttcgagg aggcccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240
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 gagtgtccat ggcaggtcct gttgtggtg aatggagctc agttgtgtgg ggggaccctg 660

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qccccatttc cc	1332

<210> 8

<211> 444

<212> PBT

<213> Homo sapiens

<400> 8

Met Val Ser

1

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Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
 50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
 100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
 115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
 130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
 180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
 195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
 210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
 225 230 235 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
 245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
 260 265 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
 420 425 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
 435 440

<210> 9

<211> 1437

<212> DNA

<213> Homo sapiens

<400> 9

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ggatatctac tcagtgctga atgtacagtt tttcttgatc atgaaaacgc caacaaaatt 120

ctgaatcgccaaagaggta	taattcaggt	aaatttggaaag	agtttgttca	aggaaacctt	180
gagagagaat	gtatggaaaga	aaagtgttgt	tttgaagaac	cacgagaagt	240
actgaaaaga	caactgaatt	tttggaaagcag	tatgttgatg	gagatcagtg	300
ccatgtttaa	atggcggcag	tttgcaggat	gacattaatt	cctatgaatg	360
tttggatttg	aaggaaagaa	ctgtgaatta	gatgtacat	gtaacattaa	420
tgcgagcagt	tttgtaaaaa	tagtgcgtat	aacaagggtgg	tttgcctctg	480
tatcgacttg	cagaaaacca	gaagtccctgt	gaaccagcag	tgccatttcc	540
gtttctgttt	cacaaacttc	taagctcacc	cgtgctgagg	ctgttttcc	600
tatgtaaatc	ctactgaagc	tgaaaccatt	ttggataaca	tcactcaagg	660
tttaatgact	tcactcgggt	ttttgggttga	gaagatgcca	aaccaggta	720
caggttgttt	tgaatggtaa	agttgatgca	tttgcgtggag	gctctatcgt	780
tggattgtaa	ctgctgccc	ctgtgttga	actgggttta	aaattacagt	840
gaacataata	tttggaggagac	agaacataca	gagcaaaagc	gaaatgtgtat	900
attcctcacc	acaactacaa	tgcagctatt	aataagtaca	accatgacat	960
gaactggacg	aacccttagt	gctaaacagc	tacgttacac	ctatgtcat	1020
gaatacacga	acatcttcct	caaatttgga	tctggctatg	taagtggctg	1080
ttccacaaag	ggagatcagc	tttagttctt	cagttaccta	gagttccact	1140
gccacatgtc	ttcgatctac	aaagttcacc	atctataaca	acatgttctg	1200
catgaaggag	gttagagattc	atgtcaagga	gatagtgggg	gaccccatgt	1260
gaagggacca	gtttcttaac	tggaatttatt	agctgggttg	aagagtgtgc	1320
aaatatggaa	tatataccaa	ggtatcccg	tatgtcaact	ggattaagga	1380
ctcacttaat	gaaagatgga	tttccaaggt	taattcattg	gaattgaaaa	1437

<210> 10

<211> 462

<212> PRT

<213> Homo sapiens

<400> 10

Met	Gln	Arg	Val	Asn	Met	Ile	Met	Ala	Glu	Ser	Pro	Ser	Leu	Ile	Thr
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Ile	Cys	Leu	Leu	Gly	Tyr	Leu	Leu	Ser	Ala	Glu	Cys	Thr	Val	Phe	Leu
					20			25				30			

Asp	His	Glu	Asn	Ala	Asn	Lys	Ile	Leu	Asn	Arg	Pro	Lys	Arg	Tyr	Asn
					35				40			45			

Ser	Gly	Lys	Leu	Glu	Glu	Phe	Val	Gln	Gly	Asn	Leu	Glu	Arg	Glu	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn		
65	70	75
80		
Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln		
85	90	95
Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile		
100	105	110
Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys		
115	120	125
Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe		
130	135	140
Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly		
145	150	155
160		
Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe		
165	170	175
Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala		
180	185	190
Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu		
195	200	205
Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe		
210	215	220
Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp		
225	230	235
240		
Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile		
245	250	255
Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly		
260	265	270
Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu		
275	280	285
His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His		
290	295	300
Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu		
305	310	315
320		
Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys		
325	330	335
Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly		
340	345	350
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu		
355	360	365
Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu		
370	375	380

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
 450 455 460

<210> 11

<211> 603

<212> DNA

<213> Homo sapiens

<400> 11

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ttcttctccc agccgggtgc cccaaatactt cagtgcattt gctgctgctt ctctagagca 180

tatcccaactc cactaaggta caagaagacg atgttggtcc aaaagaacgt cacctcagag 240

tccacttgct gtgttagctaa atcatataac agggtcacag taatgggggg tttcaaagt 300

gagaaccaca cggcgtgcca ctgcagttact ttttattttt acaaatactta aatgttttac 360

caagtgcgtt ctgtatgact gctgattttcc tggatggaa aattaagttt ttttagtgc 420

atggctttgt gagataaaac ttccttttcc ttaccatac cactttgaca cgcttcaagg 480

atataactgca gtttactgc cttccttcott atcctacagt acaatcagca gtctagttct 540

tttcatttgg aatgaataaca gcatthaagct tttccactg caaataaagc cttttaaatc 600

atc 603

<210> 12

<211> 116

<212> PRT

<213> Homo sapiens

<400> 12

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
 1 5 10 15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
 20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
 35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
 65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
 85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
 100 105 110

Tyr His Lys Ser
 115

<210> 13
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 13
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 tgtgagctga ccaacatcac cattgcaata gagaagaag aatgtcgttt ctgcataagc 120
 atcaacacca cttgggtgtgc tggctactgc tacaccaggg atctgggtgttaaaggacca 180
 gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggtatatga aacagtgaga 240
 gtgcccggct gtgctcacca tgcagattcc ttgtatacat acccagtggc caccagtgt 300
 cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggcccagc 360
 tactgctcct ttggtaat gaaagaataa 390

<210> 14
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Lys Thr Leu Gln Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
 1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
 20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
 35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
 50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
 65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
 85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
 100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys

115

120

125

Glu

<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

<400> 16
 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Arg

<210> 17
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 17
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 cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccg 120
 cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcatc 180
 tcagaaatgt ttgacctcca ggagccgacc tgcctacaga cccgcctgga gctgtacaag 240
 cagggcctgc ggggcagcct caccaagctc aagggccct tgaccatgtat ggccagccac 300
 tacaaggcagc actgcctcc aaccccgaa acttcctgtg caacccagat tatcaccttt 360
 gaaagttca aagagaacct gaaggacttt ctgcttgtca tcccctttga ctgctggag 420

ccagtccagg agtga 435

<210> 18
<211> 144
<212> PRT
<213> Homo sapiens

<400> 18
Met Trp Leu Gln Ser Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
130 135 140

<210> 19
<211> 501
<212> DNA
<213> Homo sapiens

<400> 19
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tgttactgcc aggacccata tgtaaaagaa gcagaaaaacc ttaagaaata ttttaatgca 120
ggtcattcag atgttagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180
gaggagagtg acagaaaaat aatgcagagc caaattgtct cttttactt caaacttttt 240
aaaaacttta aagatgacca gagcatccaa aagagtgtgg agaccatcaa ggaagacatg 300
aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaaa gctgactaat 360
tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgtg 420
gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480
ggtcgaagag catcccagta a 501

<210> 20
<211> 166

<212> PRT

<213> Homo sapiens

<400> 20

Met	Lys	Tyr	Thr	Ser	Tyr	Ile	Leu	Ala	Phe	Gln	Leu	Cys	Ile	Val	Leu
1						5				10				15	

Gly	Ser	Leu	Gly	Cys	Tyr	Cys	Gln	Asp	Pro	Tyr	Val	Lys	Glu	Ala	Glu
							20			25			30		

Asn	Leu	Lys	Lys	Tyr	Phe	Asn	Ala	Gly	His	Ser	Asp	Val	Ala	Asp	Asn
						35			40			45			

Gly	Thr	Leu	Phe	Leu	Gly	Ile	Leu	Lys	Asn	Trp	Lys	Glu	Glu	Ser	Asp
						50			55			60			

Arg	Lys	Ile	Met	Gln	Ser	Gln	Ile	Val	Ser	Phe	Tyr	Phe	Lys	Leu	Phe
65						70				75			80		

Lys	Asn	Phe	Lys	Asp	Asp	Gln	Ser	Ile	Gln	Lys	Ser	Val	Glu	Thr	Ile
						85			90			95			

Lys	Glu	Asp	Met	Asn	Val	Lys	Phe	Phe	Asn	Ser	Asn	Lys	Lys	Arg
						100			105			110		

Asp	Asp	Phe	Glu	Lys	Leu	Thr	Asn	Tyr	Ser	Val	Thr	Asp	Leu	Asn	Val
						115			120			125			

Gln	Arg	Lys	Ala	Ile	His	Glu	Leu	Ile	Gln	Val	Met	Ala	Glu	Leu	Ser
						130			135			140			

Pro	Ala	Ala	Lys	Thr	Gly	Lys	Arg	Lys	Arg	Ser	Gln	Met	Leu	Phe	Arg
145						150				155			160		

Gly	Arg	Arg	Ala	Ser	Gln										
					165										

<210> 21

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 21

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cctgtgctgc	ctggtccctg	tctccctggc	tgaggatccc	cagggagatg	ctgcccagaa	120
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gacagataca	tcccaccatg	atcaggatca	ccaaaccttc	aacaagatca	cccccaacct	180
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ggctgagttc	gccttcagcc	tataccgcca	gctggcacac	cagtccaaaca	gcaccaatat	240
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cttcttctcc	ccagtgagca	tcgctacagc	ctttgcaatg	ctctccctgg	ggaccaaggc	300
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tgacactcac	gatgaaatcc	tggaggccct	gaatttcaac	ctcacggaga	ttccggaggc	360
------------	------------	------------	------------	------------	------------	-----

tcagatccat	gaaggcttcc	aggaactctt	ccgtaccctc	aaccagccag	acagccagct	420
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ccagctgacc	accggcaatg	gcctgttcct	cagcgagggc	ctgaagctag	tggataagtt	480
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tttggaggat	gttaaaaagt	tgtaccactc	agaagccttc	actgtcaact	tcggggacac	540
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cgaagaggcc aagaaacaga tcaacgatta cgtggagaag ggtactcaag ggaaaattgt 600
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 taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt 720
 ggaccagggtg accaccgtga aggtgcctat gatgaagcgt ttaggcattt ttaacatcca 780
 gcactgtaag aagctgtcca gctgggtgct gctgatgaaa tacctggca atgccaccgc 840
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 tatcatcacc aagttcctgg aaaatgaaga cagaaggctt gccagcttac atttacccaa 960
 actgtccatt actggAACCT atgatctgaa gagcgtcctg ggtcaactgg gcatcactaa 1020
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 ccctggatga cattaaagaa gggttgagct gg 1352

<210> 22
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
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 Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
 20 25 30
 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 35 40 45
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 50 55 60
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 65 70 75 80
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 85 90 95
 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
 100 105 110
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 115 120 125
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 145 150 155 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 165 170 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 180 185 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 195 200 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 210 215 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
 225 230 235 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 245 250 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 260 265 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 275 280 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 290 295 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 305 310 315 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 325 330 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 355 360 365

Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 370 375 380

Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 385 390 395 400

Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 405 410 415

Gln Lys

<210> 23
 <211> 2004
 <212> DNA
 <213> Homo sapiens

<400> 23
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ggatggagtt ttcaagtccct tccagagagg aatgtcccaa gccttgagt aggttaagca	180
tcatggctgg cagcctcaca ggtttgcctc tacttcaggc agtgcgtgg gcatcaggtg	240
cccgccctg catccctaaa agcttcggct acagctcggt ggtgtgtgtc tgcaatgcca	300
catactgtga ctcccttgac ccccccaccc ttctgtccct tggtaacctc agccgctatg	360
agagtacacg cagtgggcga cggatggagc tgagtatggg gcccatccag gctaatcaca	420
cgggcacagg cctgctactg accctgcagc cagaacagaa gttccagaaa gtgaaggat	480
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aaaatttgct acttaaatcg tacttctctg aagaaggaat cggatataac atcatccggg	600
tacccatggc cagctgtgac ttctccatcc gcacctacac ctatgcagac acccctgatg	660
atttccagtt gcacaacttc agcctccag aggaagatac caagctcaag atacccctga	720
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cacccacttg gctcaagacc aatggagcgg tgaatggaa ggggtcactc aaggacagc	840
ccggagacat ctaccaccag acctggcca gatactttgt gaagttcctg gatgcctatg	900
ctgagcacaa gttacagttc tggcagtga cagctgaaaa tgagccttct gctggctgt	960
tgagtggata ccccttccag tgcctggct tcacccctga acatcagcga gacttcattt	1020
cccggtgacct aggtcctacc ctgcacaaca gtactcacca caatgtccgc ctactcatgc	1080
tggatgacca acgcttgctg ctgccccact gggcaaaggt ggtactgaca gaccagaag	1140
cagctaaata tggcatggc attgctgtac attggcacct ggactttctg gctccagcca	1200
aagccaccct aggggagaca caccgcctgt tccccaaacac catgctctt gcctcagagg	1260
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 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
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Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
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Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
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Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
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Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
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Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro

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Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys		
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Phe	Lys	Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	Gln	Leu	Gln
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Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala
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Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile
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 cctctgttgt agaaaaacta tgtgatgaaa ctttgaaaaa gatatttatg atgttaacat 7440
 ttcaggttaa gcctcatacg tttaaaataa aactctcagt tgtttattat cctgatcaag 7500
 catggaacaa agcatgttcc aggatcagat caataacaatc ttggagtcaa aaggcaaatc 7560
 atttggacaa tctgcaaaat ggagagaata caataactac tacagtaaag tctgtttctg 7620
 ctgccttaca catagatata attatgttat ttagtcatta tgaggggcac attcttatct 7680
 ccaaaactag cattctaaa ctgagaatta tagatgggt tcaagaatcc ctaagtcccc 7740
 tggaaattata taaggcattc tgtataaatg caaatgtgca ttttctgac gagtgccat 7800
 agatataaag ccatgggtc ttaattctga ccaataaaaa aataagtca gaggatgcaa 7860
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 gaaaatgtg a 7931

<210> 30
 <211> 2351
 <212> PRT
 <213> Homo sapiens

<400> 30
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 Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
 20 25 30
 Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
 35 40 45
 Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
 50 55 60
 Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
 65 70 75 80
 Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
 85 90 95
 Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
 100 105 110
 His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
 115 120 125
 Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
 130 135 140
 Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
 145 150 155 160
 Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
 165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
 180 185 190

 Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
 195 200 205

 Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
 210 215 220

 Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
 225 230 235 240

 Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
 245 250 255

 Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
 260 265 270

 Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
 275 280 285

 Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
 290 295 300

 Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
 305 310 315 320

 Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
 325 330 335

 Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
 340 345 350

 Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
 355 360 365

 Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
 370 375 380

 Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
 385 390 395 400

 Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
 405 410 415

 Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
 420 425 430

 Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
 435 440 445

 Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
 450 455 460

 Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
 465 470 475 480

 Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
 485 490 495

 His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys

500	505	510
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Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe		
515	520	525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp		
530	535	540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg		
545	550	555
560		

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu		
565	570	575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val		
580	585	590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu		
595	600	605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp		
610	615	620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val		
625	630	635
640		

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp		
645	650	655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe		
660	665	670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr		
675	680	685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro		
690	695	700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly		
705	710	715
720		

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp		
725	730	735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys		
740	745	750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg		
755	760	765

Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp		
770	775	780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys		
785	790	795
800		

Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser		
805	810	815

Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr		
820	825	830

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
 835 840 845

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
 850 855 860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
 865 870 875 880

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
 885 890 895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
 900 905 910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
 915 920 925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
 930 935 940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
 945 950 955 960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
 965 970 975

Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
 980 985 990

Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
 995 1000 1005

Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser
 1010 1015 1020

Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser
 1025 1030 1035

Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu
 1040 1045 1050

Ser Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg
 1055 1060 1065

Met Leu Met Asp Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met
 1070 1075 1080

Ser Asn Lys Thr Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln
 1085 1090 1095

Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met
 1100 1105 1110

Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile
 1115 1120 1125

Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro
 1130 1135 1140

Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu
 1145 1150 1155
 Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys
 1160 1165 1170
 Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe Pro
 1175 1180 1185
 Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu
 1190 1195 1200
 Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu
 1205 1210 1215
 Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile
 1220 1225 1230
 His Thr Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu
 1235 1240 1245
 Leu Ser Thr Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr
 1250 1255 1260
 Ala Pro Val Leu Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn
 1265 1270 1275
 Arg Thr Lys Lys His Thr Ala His Phe Ser Lys Lys Gly Glu Glu
 1280 1285 1290
 Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val Glu
 1295 1300 1305
 Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln
 1310 1315 1320
 Asn Phe Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg
 1325 1330 1335
 Leu Pro Leu Glu Glu Thr Glu Leu Glu Lys Arg Ile Ile Val Asp
 1340 1345 1350
 Asp Thr Ser Thr Gln Trp Ser Lys Asn Met Lys His Leu Thr Pro
 1355 1360 1365
 Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu Lys Gly Ala
 1370 1375 1380
 Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser
 1385 1390 1395
 Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser
 1400 1405 1410
 Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe
 1415 1420 1425
 Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys
 1430 1435 1440
 Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys

1445	1450	1455
Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu		Met Thr Gly
1460	1465	1470
Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala	Thr Asn Ser	
1475	1480	1485
Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro	Lys Pro Asp	
1490	1495	1500
Leu Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro	Lys Val His	
1505	1510	1515
Ile Tyr Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser	Asn Gly Ser	
1520	1525	1530
Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu Leu	Gln Gly Thr	
1535	1540	1545
Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro	Gly Lys Val	
1550	1555	1560
Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys	Thr Pro Ser	
1565	1570	1575
Lys Leu Leu Asp Pro Leu Ala Trp Asp Asn His Tyr	Gly Thr Gln	
1580	1585	1590
Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu Lys Ser	Pro Glu Lys	
1595	1600	1605
Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu	Asn Ala Cys	
1610	1615	1620
Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly	Gln Asn Lys	
1625	1630	1635
Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg	Thr Glu Arg	
1640	1645	1650
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His	Gln Arg Glu	
1655	1660	1665
Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu	Ile Asp Tyr	
1670	1675	1680
Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp	Phe Asp Ile	
1685	1690	1695
Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe	Gln Lys Lys	
1700	1705	1710
Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu	Trp Asp Tyr	
1715	1720	1725
Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg	Ala Gln Ser	
1730	1735	1740
Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln	Glu Phe Thr	
1745	1750	1755

Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu
 1760 1765 1770
 His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp
 1775 1780 1785
 Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser
 1790 1795 1800
 Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly
 1805 1810 1815
 Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr
 1820 1825 1830
 Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu
 1835 1840 1845
 Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu
 1850 1855 1860
 Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His
 1865 1870 1875
 Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
 1880 1885 1890
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp
 1895 1900 1905
 Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn
 1910 1915 1920
 Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His
 1925 1930 1935
 Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met
 1940 1945 1950
 Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser
 1955 1960 1965
 Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr
 1970 1975 1980
 Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr
 1985 1990 1995
 Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly
 2000 2005 2010
 Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly
 2015 2020 2025
 Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro
 2030 2035 2040
 Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala
 2045 2050 2055

Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His
 2060 2065 2070
 Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser
 2075 2080 2085
 Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile
 2090 2095 2100
 Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
 2105 2110 2115
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr
 2120 2125 2130
 Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn
 2135 2140 2145
 Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile
 2150 2155 2160
 Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg
 2165 2170 2175
 Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys
 2180 2185 2190
 Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln
 2195 2200 2205
 Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser
 2210 2215 2220
 Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp
 2225 2230 2235
 Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe
 2240 2245 2250
 Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys
 2255 2260 2265
 Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser
 2270 2275 2280
 Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys
 2285 2290 2295
 Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val
 2300 2305 2310
 Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His
 2315 2320 2325
 Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu
 2330 2335 2340
 Gly Cys Glu Ala Gln Asp Leu Tyr
 2345 2350

<211> 1471
 <212> DNA
 <213> Homo sapiens

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 cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctcgcccggc 180
 caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac 240
 agcacataca cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgtgt 300
 agctctgacc aggtggaaac tcaaggctgc actcggaaac agaaccgcac ctgcacactgc 360
 aggccggct ggtactgcgc gctgagcaag caggagggtt gccggctgtg cgccgcgtg 420
 cgcaagtgcc gcccggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg 480
 tgcaaggccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgcagg 540
 ccccaccaga tctgtaacgt ggtggccatc cctggaaatg caagcatgga tgcagtctgc 600
 acgtccacgt ccccccacccg gagtatggcc ccagggcag tacacttacc ccagccagtg 660
 tccacacgat cccaacacac gcagccaact ccagaaccca gcactgctcc aagcacctcc 720
 ttcctgctcc caatgggccc cagccccca gctgaaggga gcactggcga cttcgcttt 780
 ccagttggac tgattgtggg tgtgacagcc ttgggtctac taataatagg agtggtaac 840
 tgtgtcatca tgacccaggt gaaaaagaag cccttgcgc tgcagagaga agccaagggtg 900
 cctcacttgc ctgcccataa ggcccgggtt acacagggcc ccgagcagca gcacctgctg 960
 atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga 1020
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 gcccggccca gcaccgggag ctcagattct tcccctggtg gccatggac ccaggtcaat 1140
 gtcacctgca tcgtaacgt ctgtagcagc tctgaccaca gtcacagtg ctccctccaa 1200
 gccagctcca caatgggaga cacagattcc agcccctcg agtccccaa ggacgagcag 1260
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 <210> 32
 <211> 461
 <212> PRT
 <213> Homo sapiens

 <400> 32

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 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30
 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 35 40 45
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220
 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240
 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255
 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285
 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser

325

330

335

Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
 420 425 430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
 435 440 445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
 450 455 460

<210> 33

<211> 1475

<212> DNA

<213> Homo sapiens

<400> 33

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tcgtgagcga ctccaaaggc agcaatgaac ttcatcaagt tccatcgAAC tggactgtc 180

taaatggagg aacatgtgtg tccaaacaagt acttctccaa cattcactgg tgcaactgcc 240

caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300

atggtcactt ttaccgagga aaggccagca ctgacaccat gggccggccc tgccgtccct 360

ggaactctgc cactgtcctt cagcaaacgt accatgccc cagatctgat gctttcagc 420

tgggcctggg gaaacataat tactgcagga acccagacaa ccggaggcga ccctgggtct 480

atgtgcaggt gggcctaaag ccgcttgcac aagagtgcac ggtgcacatgc tgccgatgt 540

aaaaaaagcc ctcccttcct ccagaagaat taaaatttca gtgtggccaa aagactctga 600

ggcccccgtt taagattatt gggggagaat tcaccaccat cgagaaccag ccctggtttg 660

cggccatcta caggaggcac cggggggct ctgtcaccta cgtgtgtggg ggcagcctca 720

tcagcccttg ctgggtgatc agcgccacac actgcttcat tgattaccca aagaaggagg 780

actacatcgt ctacctgggt cgctcaaggc ttaactccaa cacgcaaggg gagatgaagt 840

ttgaggtggaa aaacctcatc ctacacaagg actacagcgc tgacacgctt gctcaccaca 900

acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgcag ccatcccgga 960
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 aagtccaccac caaaatgctg tgtgctgctg acccacagtg gaaaacagat tcctgccagg 1200
 gagactcagg gggaccctc gtctgttccc tccaaggccg catgactttg actggaattg 1260
 tgagctgggg ccgtggatgt gcccctgaagg acaagccagg cgtctacacg agagtctcac 1320
 acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggt 1380
 ccccagggag gaaacgggca ccacccgctt tcttgctgggt tgtcattttt gcagtagagt 1440
 catctccatc agctgttaaga agagactggg aagat 1475

 <210> 34
 <211> 431
 <212> PRT
 <213> Homo sapiens

 <400> 34
 Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
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 Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
 20 25 30

 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
 35 40 45

 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gln His Cys Glu Ile
 50 55 60

 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
 65 70 75 80

 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
 85 90 95

 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110

 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125

 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140

 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160

 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175

 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp

	180	185	190
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val			
195	200	205	
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His			
210	215	220	
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly			
225	230	235	240
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val			
245	250	255	
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His			
260	265	270	
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys			
275	280	285	
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr			
290	295	300	
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys			
305	310	315	320
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val			
325	330	335	
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly			
340	345	350	
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys			
355	360	365	
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu			
370	375	380	
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys			
385	390	395	400
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu			
405	410	415	
Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu			
420	425	430	
<210> 35			
<211> 107			
<212> PRT			
<213> Mus musculus			
<400> 35			
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly			
1	5	10	15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala			
20	25	30	
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile			
35	40	45	

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 36

<211> 120

<212> PRT

<213> Mus musculus

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 37

<211> 120

<212> PRT

<213> Mus musculus

<400> 37

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 38

<211> 106

<212> PRT

<213> Mus musculus

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95

Phe Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 39

<211> 1039

<212> DNA

<213> Homo sapiens

<400> 39

tcctgcacag gcagtgcctt gaagtgcctc ttccagagacc ttcttcata gactacttt 60

ttttcttaa gcagcaaaag gagaaaattg tcataaagg atattccaga ttcttgacag 120

cattctcgctc atctctgagg acatcaccat catctcagga tgagggcat gaagctgctg 180

ggggcgctgc tggcactggc ggcctactg cagggggccg tgcctctgaa gatcgagcc 240

ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 300

gtgcagatcc tgagccgcta tgacatgcc ctggtccagg aggtcagaga cagccacctg 360

actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420

gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480

cctgaccagg tgtctgcgggt ggacagctac tactacgatg atggctgcga gcccgcggg	540
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctccgggtt cacagaggtc,	600
agggagtttg ccattgttcc cctgcatgctg gccccggggg acgcagtagc cgagatcgac	660
gctctctatg acgtctaccc ggtatgtccaa gagaaatggg gcttggagga cgtcatgtt	720
atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc	780
ctgtggacaa gccccacatt ccagtggctg atccccgaca gcgctgacac cacagctaca	840
cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgcgtt	900
gttcccgact cggctttcc cttaacttc caggctgcct atggcctgag tgaccaactg	960
gccccaaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc	1020
cacaccagtt gaactgcag	1039

<210> 40

<211> 282

<212> PRT

<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu					
1	5		10		15
	10				
	15				

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr			
20	25		30
	30		

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val			
35	40		45
	45		

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp			
50	55		60
	60		

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp					
65	70		75		80
	75		80		
	80				

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn			
85	90		95
	95		

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser			
100	105		110
	110		

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn			
115	120		125
	125		

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe			
130	135		140
	140		

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly					
145	150		155		160
	155		160		
	160				

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val			
165	170		175
	175		

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn			
180	185		190
	190		

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
 195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
 210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
 225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
 245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
 260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys
 275 280

<210> 41

<211> 678

<212> DNA

<213> Mus musculus

<400> 41

gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gttcggtggc tcaagcatcc actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaaagtat gcttctgagt ctatgtctgg gatcccttcc 180

aggttagtg gcagtggatc agggacagat tttactctta gcatcaacac tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggtcg 300

gggacaaatt tggaaagtaaa agaagtgaag cttgaggagt ctggaggagg ctgggtgcaa 360

cctggaggat ccatgaaact ctccctgtgtt gcctctggat tcattttcag taaccactgg 420

atgaactggg tccgccagtc tccagagaag gggcttgagt gggttgtga aattagatca 480

aaatctatta attctgcaac acattatgctg gagtctgtga aaggaggtt caccatctca 540

agagatgatt ccaaaagtgc tgtctacctg caaatgaccg acttaagaac tgaagacact 600

ggcgtttatt actgttccag gaattactac ggttagtacct acgactactg gggccaaggc 660

accactctca cagtctcc 678

<210> 42

<211> 226

<212> PRT

<213> Mus musculus

<400> 42

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
 1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
 20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
 35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
 65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
 85 90 95

Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu
 100 105 110

Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser
 115 120 125

Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val
 130 135 140

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser
 145 150 155 160

Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg
 165 170 175

Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met
 180 185 190

Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn
 195 200 205

Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
 210 215 220

Val Ser
 225

<210> 43
<211> 450
<212> DNA
<213> Homo sapiens

<400> 43
gctgcatcat aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc 60
gcctcctgcc cctgctggcg ctgctggccc tctggggacc tgacccagcc gcagcctttg 120
tgaaccaaca cctgtgcggc tcacacctgg tgaaagctct ctacctagtg tgccgggaac 180
gaggcttctt ctacacaccc aagaccgcgc gggaggcaga ggacctgcag gtggggcagg 240
tggagctggg cgggggcctt ggtgcaggca gcctgcagcc cttggccctg gaggggtccc 300
tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg 360
agaactactg caactagacg cagccgcag gcagcccccc acccgccgccc tcctgcaccc 420
agagagatgg aataaagccc ttgaaccagc 450

<210> 44
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
 1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
 20 25 30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
 35 40 45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
 50 55 60

Gln Val Glu Leu Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
 65 70 75 80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
 85 90 95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
 100 105 110

<210> 45
 <211> 1203
 <212> DNA
 <213> Hepatitis B virus

<400> 45
 atgggagggtt ggtcttccaa acctcgacaa ggcattggga cgaatcttccat 60
 cctctggat tctttcccgaa tcaccagttt gaccctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg acttcaaccc caacaaggat cactggccag aggcaatcaa ggttaggagcg 180
 ggagacttcg ggcagggtt cacccacca cacggcggtc ttttgggtt gaggccctcag 240
 gctcaggcgca tattgacaac agtgccagca ggccttcctc ctgtttccac caatcgccag 300
 tcaggaagac agcctactcc catctctcca cctctaagag acagtcatcc tcaggccatg 360
 cagtggaaact ccacaacatt ccaccaagct ctgctagatc ccagagttag gggcctatata 420
 tttcctgctg gtggctccag ttccgaaaca gtaaaccctg ttccgactac tgtctcaccc 480
 atatcgtaa tcttctcgag gactggggac cctgcaccga acatggagag cacaacatca 540
 ggattcctag gacccctgtt cgtgttacag gccccgtttt tcttgggttac aagaatcctc 600
 acaataccac agagtctaga ctcgtggtgg acttctctca attttcttagg gggagcaccc 660
 acgtgtcctg gccaaaattt cgtgtccca acctccaatc actcaccaac ctcttgcct 720
 ccaatttgtc ctggatgtgt ctggatgtgt ttatcatatt cctcttcatc 780
 ctgctgctat gcctcatctt cttgtgggtt cttctggact accaaggat gttgcccgtt 840

tgcctctac ttccaggaac atcaactacc agcacggac catgcaagac ctgcacgatt 900
 cctgctcaag gaacctctat gttccctct tgtgctgta caaaaccttc ggacggaaac 960
 tgcacttgta ttcccatccc atcatcctgg gcttcgcaa gattcctatg ggagtgccc 1020
 tcagtcggtt tctcctggct cagttacta gtgccatttg ttcagtgggt cgcaggcctt 1080
 tccccactg tttggcttcc agttatatgg atgatgtggc attggggcc aagtctgtac 1140
 aacatcttga gtccctttt acctctatta ccaattttct tttgtctttg ggtatacatt 1200
 tga 1203
 <210> 46
 <211> 400
 <212> PRT
 <213> Hepatitis B virus
 <400> 46
 Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
 1 5 10 15
 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30
 Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45
 Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60
 Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80
 Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95
 Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110
 Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125
 Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140
 Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160
 Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175
 Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190
 Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
245 250 255

Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
370 375 380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
385 390 395 400

<210> 47

<211> 799

<212> DNA

<213> Homo sapiens

<400> 47

cgaaccactc agggcttgtt ggacagctca cctagctgca atggctacag gctccggac 60

gtccctgctc ctggcttttgc cctgctctg cctgcccgg cttcaagagg gcagtgcctt 120

cccaaccatt cccttatcca ggcctttga caacgctatg ctccgcgccc atcgtctgca 180

ccagctggcc tttgacacctt accaggagtt tgaagaagcc tatatccaa aggaacagaa 240

gtattcattc ctgcagaacc cccagaccc cctctgtttc tcagagtcta ttccgacacc 300

ctccaaacagg gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgt 360

gctcatccag tcgtggctgg agcccggtca gttcctcagg agtgtcttcg ccaacagcct 420

ggtgtacggc gcctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat 480

ccaaacgctg atggggaggg tggaaagatgg cagccccgg actgggcaga tcttcaagca 540

gacctacgc aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg 600

gctgctctac tgcttcagga aggacatgga caagggtcgag acattcctgc gcatcgtgca 660

gtgcccgtct gtggagggca gctgtggctt ctagctgccc gggtggcatc cctgtgaccc 720
 ctccccagtg cctctcctgg ccctggaagt tgccactcca gtgcccacca gccttgcct 780
 aataaaatata agttgcata 799

 <210> 48
 <211> 217
 <212> PRT
 <213> Homo sapiens

 <400> 48
 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu 1
 5 10 15

 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu 20
 25 30

 Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln 35
 40 45

 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys 50
 55 60

 Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe 65
 70 75 80

 Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys 85
 90 95

 Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp 100
 105 110

 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val 115
 120 125

 Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu 130
 135 140

 Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg 145
 150 155 160

 Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser 165
 170 175

 His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe 180
 185 190

 Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys 195
 200 205

 Arg Ser Val Glu Gly Ser Cys Gly Phe
 210 215

 <210> 49
 <211> 963
 <212> DNA
 <213> Homo sapiens

 <400> 49

atggagacag acacactcct gttatgggt ctgctgctct gggttccagg ttccactgg	60
gacgtcaggc gagggccccg gagcctgcgg ggcagggacg cgccagcccc cacgcctgc	120
gtcccggccg agtgcttcga cctgctggtc cgccactgcg tggcctgcgg gtcctgcgc	180
acgccgcggc cgaaccggc cggggccagc agccctgcgc ccaggacggc gtcagccg	240
caggagtcgg tggcgcggg ggcggcgag gcggcggtcg acaaaactca cacatgccca	300
ccgtgcccag cacctgaact cctggggga ccgtcagtct tcctttccc cccaaaaccc	360
aaggacaccc tcatgatctc ccggaccct gaggtcacat gcgtgggtgg ggacgtgagc	420
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc	480
aagacaaagc cgcggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc	540
gtcctgcacc aggactggct gaatggcaag gaggtaact gcaaggtctc caacaaagcc	600
ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag	660
gtgtacaccc tgcccccata ccggatgag ctgaccaaga accaggtcag cctgacctgc	720
ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tggcagccg	780
gagaacaact acaagaccac gcctccgtg ttggactccg acggctcctt ctccctctac	840
agcaagctca ccgtggacaa gagcagggtgg cagcagggga acgtttctc atgctccgtg	900
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccggaaa	960
tga	963

<210> 50
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 50
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg
20 25 30
Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
35 40 45
Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
50 55 60
Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
65 70 75 80
Gln Glu Ser Val Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
85 90 95
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
100 105 110

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 115 120 125

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 130 135 140

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 145 150 155 160

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 165 170 175

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 180 185 190

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 195 200 205

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 210 215 220

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 225 230 235 240

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 245 250 255

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 260 265 270

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 275 280 285

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 290 295 300

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 305 310 315 320

<210> 51

<211> 107

<212> PRT

<213> Homo sapiens

<400> 51

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
 100 105

<210> 52
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 52
 Asp Ile Gln Met Thr Gln Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 53
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 53
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

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 100 105 110

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Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
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Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
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Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
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Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
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Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala
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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
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caagggcagc tggttctggt ctggtcggat gaacacgtgg gtcacaatgt cctgtggaca	1740
tacgagatcc agttctctca ggacggtaag gctacaccc cggtcagcag gaagccatcg	1800
acccatcaacc tctttgtgtt cagcccagac acagggtctg tctctggctc ctaccgagtt	1860
cgagccctgg actactgggc ccgaccaggc cccttcgtgg accctgtgcc gtacctggag	1920
gtccctgtgc caagagggcc cccatccccg ggcaatccat ga	1962

<210> 66
 <211> 653
 <212> PRT
 <213> Homo sapiens

<400> 66
 Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Ala Ser
 1 5 10 15
 Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
 20 25 30
 Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
 35 40 45
 Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
 50 55 60
 Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
 65 70 75 80
 Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
 85 90 95
 Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
 100 105 110
 His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
 115 120 125
 Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
 130 135 140
 Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
 145 150 155 160
 Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
 165 170 175
 Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
 180 185 190
 Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
 195 200 205
 Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
 210 215 220
 Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
 225 230 235 240
 Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
 245 250 255
 Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
 260 265 270
 Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
 275 280 285
 Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val

290	295	300
Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala		
305	310	315
320		
Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn		
325	330	335
Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe		
340	345	350
Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg		
355	360	365
Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys		
370	375	380
Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln		
385	390	395
400		
Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His		
405	410	415
Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp		
420	425	430
Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala		
435	440	445
His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro		
450	455	460
Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu		
465	470	475
480		
Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro		
485	490	495
Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala		
500	505	510
Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro		
515	520	525
Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro		
530	535	540
Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr		
545	550	555
560		
Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys		
565	570	575
Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr		
580	585	590
Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser		
595	600	605
Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp		
610	615	620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
 625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
 645 650

<210> 67
 <211> 1290
 <212> DNA
 <213> Homo sapiens

<400> 67
 atgcagctga ggaacccaga actacatctg ggctgcgcgc ttgcgcctcg cttcctggcc 60
 ctcgtttcct gggacatccc tggggctaga gcactggaca atggattggc aaggacgcct 120
 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
 gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctcagaaggc 240
 tggaaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga 300
 gattcagaag gcagacttca ggcagaccct cagcgcttcc ctcatggat tcggcagcta 360
 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420
 acctgogcag gcttccctgg gagttttgga tactacgaca ttgatgccc gacccttgct 480
 gactggggag tagatctgct aaaatttgat ggttgttact gtgacagttt ggaaaatttg 540
 gcagatggtt ataaggcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
 tcctgtgagt ggcctcttta tatgtggccc tttcaaaagc ccaattatac agaaatccga 660
 cagtactgca atcactggcg aaattttgct gacattgtatg attcctggaa aagtataaag 720
 agtatcttgg actggacatc ttttaaccag gagagaattt ttgatgttgc tggaccaggg 780
 ggttggaatg acccagatat gttatgtattt ggcaactttt gcctcagctg gaatcagcaa 840
 gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900
 cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960
 caggaccctt tggcaagca aggttaccag ctttagacagg gagacaactt tgaatgtgg 1020
 gaacgacctc tctcaggctt agcctggct gtagctatga taaaccggca ggagattgg 1080
 ggacctcgct ctataccat cgcaatgtct tccctggta aaggagtgcc ctgtaatcct 1140
 gcctgcttca tcacacagct cttccctgtt aaaaaggaaagc tagggttcta tgaatggact 1200
 tcaaggtaa gaagtccacat aaatcccaca ggcactgttt tgcttcagct agaaaataca 1260
 atgcagatgt cattaaaaga cttaactttaa 1290

<210> 68
 <211> 429
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
 1 5 10 15
 Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240
 Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
 245 250 255
 Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
 260 265 270
 Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
 275 280 285
 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300
 Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
 420 425

<210> 69

<211> 351

<212> DNA

<213> Homo sapiens

<400> 69

atggattact acagaaaata tgcagctatc tttctggtca cattgtoggt gtttctgcat 60

gttctccatt ccgctcctga tgcaggat tgcccagaat gcacgctaca ggaaaaccca 120

ttcttcctcc agccgggtgc cccaatactt cagtgcattt gctgctgctt ctctagagca 180

tatcccactc cactaaggc caagaagacg atgttggtcc aaaagaacgt cacccagag 240

tccacttgct gtgtagctaa atcatataac agggtcacag taatgggggg tttcaaagtg 300

gagaaccaca cggcgtgcca ctgcagttact tgcattttatc acaaatttta a 351

<210> 70

<211> 116

<212> PRT

<213> Homo sapiens

<400> 70

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
 1 5 10 15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
 20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
 35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
 65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
 85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
 100 105 110

Tyr His Lys Ser
 115

<210> 71
 <211> 498
 <212> DNA
 <213> Homo sapiens

<400> 71
 atggagatgt tccagggct gctgctgttg ctgctgctga gcatggcg gacatggca 60
 tccaaggagc cgcttcggcc acgggtccgc cccatcaatg ccaccctggc tgtggagaag 120
 gagggtcgcc ccgtgtgcat caccgtcaac accaccatct gtgcccgtcta ctgccccacc 180
 atgaccgcg tgctgcaggg ggtcctgccc gcccctgcctc aggtggtgtg caactaccgc 240
 gatgtgcgt tcgagtccat ccggctccct ggctgcccgc gcccgtgaa ccccggtggc 300
 tcctacgccc tgctctcag ctgtcaatgt gcaactctgcc gccgcagcac cactgactgc 360
 gggggtccca aggaccaccc cttgacctgt gatgacccccc gcttccagga ctccctttcc 420
 tcaaaggcccc ctccccccag cttccaagc ccatccccac tccgggggcc ctccggacacc 480
 ccgatcctcc cacaataa 498

<210> 72
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 72
 Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly
 1 5 10 15

Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
 20 25 30

Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
 35 40 45

Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val
 50 55 60

Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
 65 70 75 80

Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
 85 90 95

Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
 100 105 110

Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu

115	120	¹²⁵ 125
Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro		
130	135	140
Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr		
145	150	155
Pro Ile Leu Pro Gln		
165		
<210> 73		
<211> 165		
<212> PRT		
<213> Homo sapiens		
<400> 73		
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu		
1	5	10
15		
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His		
20	25	30
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe		
35	40	45
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp		
50	55	60
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu		
65	70	75
80		
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp		
85	90	95
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu		
100	105	110
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala		
115	120	125
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val		
130	135	140
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala		
145	150	155
160		
Cys Arg Thr Gly Asp		
165		
<210> 74		
<211> 588		
<212> DNA		
<213> Homo sapiens		
<400> 74		
atggccctcc tggccctct actggcagcc ctagtcatga ccagctatag ccctgttggaa 60		
tctctggct gtgatctgcc tcagaaccat ggcctactta gcaggaacac cttggtgctt 120		
ctgcaccaaa tgaggagaat ctcccctttc ttgtgtctca aggacagaag agacttcagg 180		

ttcccccaagg agatggtaaa agggagccag ttgcagaagg cccatgtcat gtctgtcctc 240
 catgagatgc tgcagcagat cttcagcctc ttccacacag agcgctcctc tgctgcctgg 300
 aacatgaccc tcotagacca actccacact ggacttcatc agcaactgca acacctggag 360
 acctgcttgc tgcaggtagt gggagaagga gaatctgctg gggcaattag cagccctgca 420
 ctgaccttga ggaggtactt ccagggaaatc cgtgtctacc tgaaagagaa gaaatacago 480
 gactgtgcct gggaaagttgt cagaatggaa atcatgaaat cttgttctt atcaacaaac 540
 atgcaagaaa gactgagaag taaagataga gacctggct catcttga 588

 <210> 75
 <211> 195
 <212> PRT /
 <213> Homo sapiens

 <400> 75
 Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
 1 5 10 15

 Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
 20 25 30

 Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
 35 40 45

 Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
 50 55 60

 Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
 65 70 75 80

 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
 85 90 95

 Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
 100 105 110

 His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
 115 120 125

 Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
 130 135 140

 Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
 145 150 155 160

 Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
 165 170 175

 Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
 180 185 190

 Gly Ser Ser
 195